

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, February 07, 2006 7:17 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: rush search for App. #: 10/036,568

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

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FEB - 8 2006
STIC-BIOTECH/ChemLib

-----Original Message-----

From: Basi, Nirmal
Sent: Tuesday, February 07, 2006 7:16 PM
To: Chan, Christina
Subject: rush search for App. #: 10/036,568

Christina I am seeking approval for a RUSH sequence search for this amended case, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70.

Sequence search:

App. #: 10/036,568
Result format: Paper.

Title: **NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME**

Inventors: Willson et al

Priority Date: 10/23/1996

Please search:

- i) SEQ ID NO:4
- ii) Polypeptide comprising amino acids 26-426 of SEQ ID NO:4
- iii) Polypeptide comprising amino acids 26-345 of SEQ ID NO:4

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Search issued, commercial and interference databases.

Thanks,
Nirmal S. Basi

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 22:06:20 ; Search time 35.2833 Seconds
(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLLCAGG.....QTKETDSVLIENLKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2320	100.0	426	2	US-09-688-286D-4
2	2309.5	99.5	427	2	US-08-969-125-9
3	2309.5	99.5	427	2	US-09-545-002-9
4	2309.5	99.5	427	2	US-09-949-016-6094
5	1878	80.9	405	2	US-09-828-995B-50
6	1875.5	80.8	793	2	US-09-313-942-32
7	1875.5	80.8	793	2	US-10-282-162-32
8	1779.5	76.7	784	2	US-09-313-942-30
9	1779.5	76.7	784	2	US-10-282-162-30
10	1769	76.2	322	2	US-09-825-561A-82
11	1696	73.1	424	2	US-09-688-286D-2
12	1265	54.5	233	2	US-09-949-016-8550
13	329	14.2	386	2	US-09-828-995B-61
14	318	13.7	398	1	US-07-757-390-6
15	318	13.7	398	1	US-08-442-282-6
16	318	13.7	398	1	US-08-442-281-6
17	318	13.7	398	1	US-08-939-727-6
18	318	13.7	415	1	US-07-757-390-5
19	318	13.7	415	1	US-08-442-282-5
20	318	13.7	415	1	US-08-442-281-5
21	318	13.7	415	1	US-08-939-727-5
22	318	13.7	415	2	US-09-886-319A-23
23	310	13.4	365	2	US-09-828-995B-66
24	304.5	13.1	561	2	US-09-828-995B-72
25	303.5	13.1	561	2	US-09-828-995B-81
26	297	12.8	565	2	US-09-828-995B-75
27	296.5	12.8	420	2	US-09-886-319A-24

28	296.5	12.8	420	2	US-09-949-016-5958	Sequence 5958, Ap
29	296	12.8	318	2	US-09-828-995B-69	Sequence 69, Appl
30	296	12.8	563	2	US-09-828-995B-78	Sequence 78, Appl
31	294.5	12.7	380	1	US-08-609-572-4	Sequence 4, Appl
32	294.5	12.7	380	2	US-08-841-751-4	Sequence 4, Appl
33	294.5	12.7	380	2	US-08-846-340-4	Sequence 4, Appl
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39	294.5	12.7	420	1	US-08-939-727-13	Sequence 8614, Ap
40	293.5	12.7	427	2	US-09-949-016-8614	Sequence 8620, Ap
41	293.5	12.7	427	2	US-09-949-016-8620	Sequence 2, Appl
42	287.5	12.4	383	1	US-08-609-572-2	Sequence 2, Appl
43	287.5	12.4	383	2	US-08-841-751-2	Sequence 2, Appl
44	287.5	12.4	383	2	US-08-846-340-2	Sequence 2, Appl
45	287.5	12.4	383	2	US-08-846-344-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

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Best Local Similarity	100.0%	Pred. No. 5.2e-220;		
Matches 426;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	61	CSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVQVSGQCSNTESEKPSILVEKICISPP	120	
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DB	121	EGDPESAVTELQCIWHNLSYMKCSMLPGNTSPDNTYTYWHRSLKTHQENIFREGQ	180	
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DB	181	YFGCSFDLTWKVQSSFEQHSQVIMVKDNAGKIKPSNIVPLTSRVKPDPPHINKLSFHD	240	
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Db 241 DLYVQWENPQNFISRCLFYEVVNNSTQTHNVFVQEAECNPEFERNVENTSCFMVPG 300
Qy 301 VLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKNSTLYITMLLIIVPVIAGAI 360
Db 301 VLPDTLNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 361 VLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDLTLHWKDYDIYEKQTEETDSVLLIEN 420
Db 361 VLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDLTLHWKDYDIYEKQTEETDSVLLIEN 420
Qy 421 LKXASQ 426
Db 421 LKXASQ 426

RESULT 2
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 61 NCSLWTFSHFGDKQDKKIAPIARRSRSEIPLNERICLVQVGCSTNSEKPSILVEKICSP 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQENIFREG 179

Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQENIFREG 180
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Db 181 QYFGCSFDLTQVDSFEQSHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVVNNSTQTHNVFVQEAECNPEFERNVENTSCFMVPG 299
Db 241 DDLYVQWENPQNFISRCLFYEVVNNSTQTHNVFVQEAECNPEFERNVENTSCFMVPG 300
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Db 301 GVLPTLNTVIRVKTNKLCEYEDDKLWSNWSQMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDLTLHWKDYDIYEKQTEETDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPPIPDGKIFKEMFGQNDLTLHWKDYDIYEKQTEETDSVLLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427

RESULT 3
US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MEWPARLCGLWALLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTVNPPGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVQVSCQSTNESEKPSILVEKCI 119
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Db 121 PGDPESAATVTELOCIWHLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCE 180
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Db 301 GVLDPDTLNTVIRVKTNKLKCYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPV 360
QY 360 IVLLLYLKRLLKIIIPPPIDPGKIPKEMFGQNDTTLHWKYDYIEKQTKETSDSV 419
Db 361 IVLLLYLKRLLKIIIPPPIDPGKIPKEMFGQNDTTLHWKYDYIEKQTKETSDSV 420
QY 420 NLKQASQ 426
Db 421 NLKQASQ 427
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US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6094
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 5.6e-219;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARLCGLWALLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTVNPPGASS 59
Db 1 MEWPARLCGLWALLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTVNPPGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVQVSCQSTNESEKPSILVEKCI 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLVQVSCQSTNESEKPSILVEKCI 120
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Db 121 PGDPESAATVTELOCIWHLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQCE 180
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Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTQTHNVFYVQEAECENPEFERNVENTSC 300
QY 300 GVLDPDTLNTVIRVKTNKLKCYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPV 359
Db 301 GVLDPDTLNTVIRVKTNKLKCYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPV 360
QY 360 IVLLLYLKRLLKIIIPPPIDPGKIPKEMFGQNDTTLHWKYDYIEKQTKETSDSV 419
Db 361 IVLLLYLKRLLKIIIPPPIDPGKIPKEMFGQNDTTLHWKYDYIEKQTKETSDSV 420
QY 420 NLKQASQ 426
Db 421 NLKQASQ 427
RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50
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Best Local Similarity 85.2%; Pred. No. 1.9e-176;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
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QY 82 RRSIEVPLNERICLVQVSCQSTNESEKPSILVEKICISPEGDPESAATVTELOCIWHLN 141
Db 61 HRSKEVPLNERICLVQVSCQSTNESEKPSILVEKCTPPPEGDPESAATVTELOCIWHLN 120
QY 142 KCSWLPGRNTSPDTNTLYYWHRSLEKIHQCEINIFREGQYFCGCSFDLTAKVQDSSFEQHSV 201
Db 121 KCTWLPGRNTSPDTNTLYYWHSSLGKILQCEDIYREGQHIQCSFALTNLKDSSFEQHSV 180
QY 202 QIMVKDNAGKIKPSFNIPLTSRVKPDPPHIIKNLSFHNDDLVQWENPQNFISRCIFYE 261
Db 181 QIMVKDNARKIRPSFNIPLTSRVKPDPPHIIKRLFFQGNLVQWKNPQNFISRCIFYE 240
QY 262 EVNNSQTHNVFYVQEAECENPEFERNVENTSCFWPGVLPDPTLNTVIRVKTNKL 321
Db 241 EVNNSQTHNDIFYVEBAKQCNSEGNLEGTCFVWPGVLPDPTLNTVIRVKTNKL 300
QY 322 DDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAILVLLLYLKRLLKIIIPPPIDPG 381
Db 301 DDKLSNWSQAMSIGENTDPTFYITWLLATQVIVAGAILLLLYLKRLLKIIIPPPIDPG 360
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Db 361 KIFKEMFGDNDTLLHWKDYIEKQKKESTDSVLIENLKASQ 405

RESULT 6
US-09-313-942-32
; Sequence 32, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match 80.8%; Score 1875.5; DB 2; Length 793;
Best Local Similarity 99.4%; Pred. No. 9.1e-176;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKCI 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKCI 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKTHQENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKTHQENIFREG 180
Qy 180 QYFGCSFDLTVKVDSSPEQHSQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTVKVDSSPEQHSQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQBAKCNPFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQBAKCNPFERNVENTSCFMVP 300
Qy 300 GVLPLDTLNTVIRVKTNKLCEYDDDKLWSNWSQMSIGKKRNST 342
Db 301 GVLPLDTLNTVIRVKTNKLCEYDDDKLWSNWSQMSIGKKRNST 343

RESULT 8
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match 76.7%; Score 1779.5; DB 2; Length 784;
Best Local Similarity 90.4%; Pred. No. 2.6e-166;
Matches 328; Conservative 5; Mismatches 15; Indels 15; Gaps 2;

Qy 20 GGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAP 79
Db 233 GGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKQDKKIAP 292
Qy 80 ETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKCI 139
Db 293 ETRRSIEVPLNERICIQVGSQCSTNESEKPSILVEKCI 352
Qy 140 YMKCSWLPGRNTSPDNTYTYWHRSLKTHQENIFREGQYFGCSFDLTVKVDSSPEQHSQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 199

Qy 382 KIFKEMFGDNDTLLHWKDYIEKQKKESTDSVLIENLKASQ 426
Db 361 KIFKEMFGDNDTLLHWKDYIEKQKKESTDSVLIENLKASQ 405

RESULT 6
US-09-313-942-32
; Sequence 32, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
```

Db 353 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFQH 412
Qy 200 SVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 259
Db 413 SVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 472
Qy 260 EVEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 319
Db 473 EVEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 532
Qy 320 YEDDKLWSNWSQEMSIGKGRNST----LYITWMLLIVPVIVAGAIIVLLLYLKRKLIIIPP 375
Db 533 YEDDKLWSNWSQEMSIGKGRNSTTGDKTHTCCPCPAPELLGSP-----SVFLFP 581
Qy 376 PIP 378
Db 582 PKP 584
RESULT 9
US-10-282-162-30
; Sequence 30, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30
Query Match 76.7%; Score 1779.5; DB 2; Length 784;
Best Local Similarity 90.4%; Pred. No. 2.6e-166;
Matches 328; Conservative 5; Mismatches 15; Indels 15; Gaps 2;
Qy 20 GGGGGAPTETPTOPPTNLSVSVENLCTVIWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 79
Db 233 GGGGGAAPTETPTOPPTNLSVSVENLCTVIWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 292
Qy 80 ETRRSIEVPLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLS 139
Db 293 ETRRSIEVPLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLS 352
Qy 140 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFQH 199
Db 353 YMKCSWLPGRNTSPDNTYLYWHSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFQH 412
Qy 200 SVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 259
Db 413 SVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 472
Qy 260 EVEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 319
Db 473 EVEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 532
Qy 320 YEDDKLWSNWSQEMSIGKGRNST----LYITWMLLIVPVIVAGAIIVLLLYLKRKLIIIPP 375
Db 533 YEDDKLWSNWSQEMSIGKGRNSTTGDKTHTCCPCPAPELLGSP-----SVFLFP 581
Qy 376 PIP 378
|

Db 582 PKP 584
RESULT 10
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82
Query Match 76.2%; Score 1769; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 7.4e-166;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 21 GGGGAPTETPTOPPTNLSVSVENLCTVIWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 80
Db 1 GGGGAAPTETPTOPPTNLSVSVENLCTVIWNPPEGASSNCSLWYFSGHFGDKQDKKIAP 60
Qy 81 TRRSIEVPLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLS 140
Db 61 TRRSIEVPLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLS 120
Qy 141 MKCSWLPGRNTSPDNTYLYWHSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFQH 200
Db 121 MKCSWLPGRNTSPDNTYLYWHSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFQH 180
Qy 201 VOIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 260
Db 181 VOIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCIFY 240
Qy 261 VEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 320
Db 241 VEVNSQTEHNVFYQEAKECENPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLK 300
Qy 321 EDDKLWSNWSQEMSIGKGRNST 342
Db 301 EDDKLWSNWSQEMSIGKGRNST 322
RESULT 11
US-09-688-286D-2
; Sequence 2, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10

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; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PF2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-286D-2

Query Match      73.1%; Score 1696; DB 2; Length 424;
Best Local Similarity 74.8%; Pred. No. 1.8e-158;
Matches 318; Conservative 40; Mismatches 65; Indels 2; Gaps 2;

Qy  1  MWPRLCGLWALLCAGGGGGGAPTETQPPVTNLSVVENLCTVIWTWNPPEGASN 60
Db  1  MARPALLGELLVLLLTATVGVAAA--TEVQPPVTNLSVVENLCTVIWTWSPPEGASN 59

Qy  61  CSLWYFSHFQDKQDKKIAPETRRIEVLNERICLVGSCSTNESEKPSILVEKCI 120
Db  60  CTLYFSHFDDQDKKIAPETHRKEELPLDEKICLVGSCSANESEKPSPLVKKCI 119

Qy  121  EGPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTLYYHRSLEKIHQCNIFREGQ 180
Db  120  EGPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTLYYHRSLEKIHQCNIFREGQ 179

Qy  181  YFGCSFDLTVKDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSF 240
Db  180  HIACSFKLTIV--SPSFQNVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSF 238

Qy  241  DLVQWENPQNFISRCILFYEVVNNSTQETHNVFYQAKCENPEFERNVENTSCFMV 300
Db  239  ALLVQWKNPQNFISRCILFYEVVNNSTQETHNVFYQAKCENPEFERNVENTSCFMV 298

Qy  301  VLPDTLTVIRVTKNKLCEYDDKLSNWSQESIGKRNSTLYITMLLVIPVIVAGAI 360
Db  299  VLADAVTVRVVTKNKLCEYDDKLSNWSQESIGKRNSTLYITMLLVIPVIVAVI 358

Qy  361  VLLYLLKRLKIIIPPIPDGKIFKEMFGQNDTLHWKKYDIYEKOTKEETISVVL 420
Db  359  ILLYLLKRLKIIIPPIPDGKIFKEMFGQNDTLHWKKYDIYEKOTKEETISVVL 418

Qy  421  LKKAAS 425
Db  419  LKKAAS 423

RESULT 12
US-09-949-016-8550
; Sequence 8550; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
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; ORGANISM: Human
US-09-949-016-8550

Query Match      54.5%; Score 1265; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  76  KIAPETRRIEVLNERICLVGSCSTNESEKPSILVEKCI 135
Db  1  KIAPETRRIEVLNERICLVGSCSTNESEKPSILVEKCI 60

Qy  136  HNLNLSYMKCSWLPGRNTSPDNTLYYHRSLEKIHQCNIFREGQFGCSFDLTVKDSS 195
Db  61  HNLNLSYMKCSWLPGRNTSPDNTLYYHRSLEKIHQCNIFREGQFGCSFDLTVKDSS 120

Qy  196  FEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF 255
Db  121  FEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF 180

Qy  256  CLFYEVVNNSTQETHNVFYQAKCENPEFERNVENTSCFMVGPVLPDTL 306
Db  181  CLFYEVVNNSTQETHNVFYQAKCENPEFERNVENTSCFMVGPVLPDTL 231

RESULT 13
US-09-828-995B-61
; Sequence 61; Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE Igg AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-61

Query Match      14.2%; Score 329; DB 2; Length 386;
Best Local Similarity 26.3%; Pred. No. 9.9e-24;
Matches 109; Conservative 62; Mismatches 171; Indels 72; Gaps 19;

Qy  10  LWALLCAGGGGGGAPTETQPPVTNLSVVENLCTVIWTWNP--EGASSNCSLWY-- 65
Db  11  LYTLLVCTAGSMLSNAEIKVNPQDFEIVDGVLSLQWQPLPDPNFKECTIEVEL 70

Qy  66  -FSHFGDKQDKIAP-----ETRRSIEVLNERICLVGSCSTNESEKPSILVEK 115
Db  71  KYRNIDSNNWKTITIKNLHYKDGFDLNLKGIEAKINTLL-----PAQC-TNGSEVRSSWAET 125

Qy  116  CI-SPPEGOPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTLYYHRSLEKIHQCN 174
Db  126  TYWTSPQGNRETKIQMDCCVYINWQYLVCSWKFGMVHFDNTVQLFWYGLDHSAC 185

Qy  175  IFR-EGQYFGCSFDLTVKDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPD 233
Db  186  YIKVGNKNGCRFPY--LESSDYKDFYICVNGSSESQPIRPSYIFQIQNVKMPDYL 243

Qy  234  NLSFHN--DDLQWENPQNF--SRCLFYEVVNNSTQETHNVFYQAKCENPEFERN 289
Db  244  SLTVKNSSEINLKNMPPKGPAPKACFIYEIETFGDTTWTVTV-----ENEIQ 292

Qy  290  VENTS-----CFMVGPVLPDTLTVIRVKTNKLCEYDDKLSNWSQESIGK--KRN 340
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Mon Feb 13 13:13:53 2006

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Db 293 ITRSNESQKLCFLV-----RSKNYIC-SDDGWSEMSDEQCWKGDWNET 338
Qy 341 STLVTMLLVVIVAGAIIVLLYLKR--LKIIIPPPDPGKIFKEMFGDQN 392
Db 339 LVFELIPPAFVSIFVL-VITCLLYKQKALLKTIHTK-----KEVFSHOD 383

RESULT 14
US-07-757-390-6
; Sequence 6, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-757-390-6

Query Match 13.7%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.3e-22;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 32 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWTFPSHF-GDKQDKKIAPETRRSIEVPL 89
Db 12 PPV-NFTIKATGLAQLVLLHWDNPQEQRHVDLEYHVKINAPQDEYDTRKTESKCVTPL 70
Qy 90 NERICLOVGSQCSTNESEKPSILVEKCTSPPEGDPDESATVTELCIWHNL----- 138
Db 71 HEGFAASVRTILKSHSTTLASSWSAELKAPPGSGTSTNLTCTTHTVSSHTHLRPVQ 130
Qy 139 SYMKCSWLPGRNTSPDNTYLYWHRSLKIHQCNIPRE--GOYFGCSFDLTWKVDSF 196
Db 131 VSLRCTLWVGKQADPDTQFLYRFGVLTE--KCQYSDALNRNTACHWPTFTFNSKGF 188
Qy 197 EQHSVQIMVKDAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDLQVQWENPON-FISR 255
Db 189 EQLAVHINGSKRAAKKPFQDLFSLAIDQVNPRTVVEIESNLSIYQWEKPLSAFPDH 248
Qy 256 CLFYEVENVNSQTETHNVFYQBAKCNPEFERNVENTSCFMPVGVLPDTLNTVIRVKT 315

Db 249 CFNYELKIYNTKNG-----HIQEKLIANKFISKIDDVSTY-----SIQVRAAV 292
Qy 316 NKLCYEDDKLWSNQSEMSIGKKNSTLYITMLLVIVVAGAIIVLLLYLKRLLKII--- 372
Db 293 SSPCRMPGR-WGWSQFIYVGKERS-LVFWHLIVLP---TAACFVLLISLCIVCHLW 347
Qy 373 --IPPPIDPGKIFKEMFGDQNDTDLHWKKYDIYEKQTKETSDSV 416
Db 348 TRLPPVPAPKSNIKDL-----PVVTEYEKPSNETKIEW 382

RESULT 15
US-08-442-282-6
; Sequence 6, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-6

Query Match 13.7%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.3e-22;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 32 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWTFPSHF-GDKQDKKIAPETRRSIEVPL 89
Db 12 PPV-NFTIKATGLAQLVLLHWDNPQEQRHVDLEYHVKINAPQDEYDTRKTESKCVTPL 70
Qy 90 NERICLOVGSQCSTNESEKPSILVEKCTSPPEGDPDESATVTELCIWHNL----- 138
Db 71 HEGFAASVRTILKSHSTTLASSWSAELKAPPGSGTSTNLTCTTHTVSSHTHLRPVQ 130
Qy 139 SYMKCSWLPGRNTSPDNTYLYWHRSLKIHQCNIPRE--GOYFGCSFDLTWKVDSF 196
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Db 131 VSLRCTWLVGKAPEDTQYFLYYRFGVLTB--KCQEYSRDALNRNTACWFPRTFINSKGF 188
Qy 197 EQHSVQIMVNDNAGKIKPSPNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPON-FISR 255
Db 189 EQLAVHINGSKRAAIKPPDQLFPLAIDQVNPVRNVTVIEGNSLYIQWEKPLSAPPDH 248
Qy 256 CLFYEVEVNNSTETHNVFYQEAACENPFRNVENTSCFMVPGVLPDTLNTVRIKVT 315
Db 249 CFNYELKIYNTKG-----HIQKEKLIANKPISKIDDVSTY-----SIQVRAAV 292
Qy 316 NKLCYEDDKLWSNWSQMSIGKRNSTLYITMLLIVFVIVAGAIIVLLLYLKLKII--- 372
Db 293 SSPCRMFR-WGEWSQPIYVGKERKS-LVEWHLIVLP---TAACFVLLIESLICRVCHLW 347
Qy 373 --IFPPIPDPGKIFKEMFGQNDTLHWKKYDIYEKQTKETDSVV 416
Db 348 TRLFPVPVPAPKSNIKDL-----PVTVEYKPSNETKIEW 382
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Job time : 36.2833 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 ; Search time 131.105 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLCAGGG.....QTKETDVSVLINLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2320	100.0	426	2 AAW09822	Aaw09822 Human int
2	2309.5	99.5	427	2 AAW24973	Aaw24973 Human int
3	2309.5	99.5	427	4 AAB19807	Aab19807 Human int
4	2309.5	99.5	427	8 ADL171812	Adl171812 Human int
5	2309.5	99.5	427	8 ADL182843	Adl182843 Human PRO
6	2309.5	99.5	427	8 ADN04504	Adn04504 Antipsori
7	2309.5	99.5	427	8 ADM62575	Adm62575 Human int
8	2309.5	99.5	427	8 ABM822441	Abm822441 Tumour-as
9	2303.5	99.3	427	8 ADL171813	Adl171813 Human int
10	2302.5	99.2	427	7 ADF17835	Adf17835 Human IL-
11	2302.5	99.2	427	8 ADL171814	Adl171814 Human int
12	2296.5	99.0	427	4 AAB19808	Aab19808 Human int
13	2230.5	96.1	414	8 AAX97531	Aax97531 Pancreat
14	1878	80.9	405	4 AAU69132	Aau69132 Canine in
15	1875.5	80.8	793	3 AAY92208	Aay92208 IL-13/IL-
16	1875.5	80.8	793	7 ABW02181	Abw02181 Human IL-
17	1784.5	76.9	664	7 ADF17841	Adf17841 Chimeric
18	1779.5	76.7	784	3 AAY92207	Aay92207 IL-13/IL-
19	1779.5	76.7	784	7 ABW02180	Abw02180 Human IL-
20	1769	76.2	322	5 AAEL13745	Aael13745 Human sol
21	1714	73.9	426	2 AAW09821	Aaw09821 Mouse int
22	1696	73.1	424	9 ADX97888	Adx97888 Murine IL
23	1536	66.2	286	4 AAB90678	Aab90678 Human DA1
24	942	40.6	177	2 AAW58987	Aaw58987 Homo sapi

25	465	20.0	134	8 ADP84617	Adp84617 Human bre
26	463	20.0	172	8 ADP84616	Adp84616 Human bre
27	463	20.0	226	8 ADQ5618	Adq5618 Novel hum
28	414.5	17.9	82	8 ADO26844	Ado26844 Human rec
29	329	14.2	386	4 AAU69135	Aau69135 Canine in
30	318	13.7	398	2 AAR22212	Aar22212 Sequence
31	318	13.7	415	2 AAR22211	Aar22211 Sequence
32	318	13.7	415	2 AAR22217	Aar22217 Sequence
33	318	13.7	415	5 ADZ58697	Adz58697 Mouse IL-
34	310	13.4	365	4 AAU69136	Aau69136 Canine in
35	304.5	13.1	561	4 AAU69138	Aau69138 Canine IL
36	303.5	13.1	561	4 AAU69141	Aau69141 Canine IL
37	302	13.0	372	2 AAW36616	Aaw36616 Celebus m
38	297	12.8	565	4 AAU69139	Aau69139 Canine IL-
39	296.5	12.8	420	5 ADZ58698	Adz58698 Human IL-
40	296.5	12.8	421	2 AAR25064	Aar25064 Human IL-
41	296	12.8	318	4 AAU69137	Aau69137 Canine IL
42	296	12.8	563	4 AAU69140	Aau69140 Canine IL
43	294.5	12.7	380	2 AAW36613	Aaw36613 Human bcy
44	294.5	12.7	380	2 AAW35295	Aaw35295 Human IL-
45	294.5	12.7	380	2 AAW24972	Aaw24972 Human int

ALIGNMENTS

RESULT 1
AAW09822
ID AAW09822 standard; protein; 426 AA.
XX
AC AAW09822;
XX
DT 15-JUL-1997 (first entry)
XX
DE Human interleukin-12 receptor alpha chain NR4.
XX
KW NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine;
XX allergy; asthma; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT Protein 28..426 /label= Sig_peptide
FT Domain 28..118 /label= Mat_protein
FT Modified-site 36 /label= N-glycosylation site
FT Modified-site 104 /label= N-glycosylation_site
FT Domain 119..342 /label= Haemoreceptor_receptor-domain
FT Modified-site 137 /label= N-glycosylation site
FT Region 326..330 /label= WSDWS_motif
FT Domain 343..366 /label= Transmembrane_domain
FT Domain 367..426 /label= Cytoplasmic_tail
XX
WO9715663-A1.
XX
PD 01-MAY-1997.
XX
PF 23-OCT-1996; 96WO-AU0000668.
XX
PR 23-OCT-1995; 95AU-00006135.
PR 22-DEC-1995; 95AU-00007276.
PR 09-SEP-1996; 96AU-00002208.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PA Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX PI WPI; 1997-259018/23.
XX DR N-PSDB; AAT66165.
XX DR DNA encoding animal haemopoietin receptor which interacts with
XX PT interleukin-13 - useful to treat asthma, allergy or condition exacerbated
XX FT by IGE production.
XX PS Claim 5; Page 52-54; 93pp; English.
XX CC Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),
XX CC designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
XX CC The human NR4 amino acid sequence was deduced from a composite DNA
XX CC sequence (AAT66165) derived from bone marrow cDNA clones. Recombinant
XX CC NR4, or fusion proteins including NR4, can be produced in transformed
XX CC host cells. The receptor molecules and their components are useful in the
XX CC development of a range of agonists, antagonists, therapeutics and
XX CC diagnostic reagents based on ligand interaction with its receptor, esp.
XX CC for the development of cpds. capable of modulating the activity of IL-13
XX CC and related cytokines such as interleukin-4 for the treatment of allergy,
XX CC asthma and other conditions relating to IGE
XX SQ Sequence 426 AA;
Query Match 100.0%; Score 2320; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 4.4e-212;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEWPARGLWALLLCAGGGGGGGAAPTETPPVTNLSVSVENLCTVIWTNPPGASSN 60
DB 1 MEWPARGLWALLLCAGGGGGGGAAPTETPPVTNLSVSVENLCTVIWTNPPGASSN 60
QY 61 CSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 120
DB 61 CSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 120
QY 121 EGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNLTYYWHRSLKIHQCEINFREG 180
DB 121 EGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNLTYYWHRSLKIHQCEINFREG 180
QY 181 YFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSEFNIVPLTSRVKPDPPHINKLSFHND 240
DB 181 YFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSEFNIVPLTSRVKPDPPHINKLSFHND 240
QY 241 DLYVQWENPQNFISRCIFYEVEVNNSTQETHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
DB 241 DLYVQWENPQNFISRCIFYEVEVNNSTQETHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
QY 301 VLPDPTLNTVRIKVTNKLKCYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
DB 301 VLPDPTLNTVRIKVTNKLKCYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
QY 361 VLLLYLKLRLKIIIFPPIDPGKIFKEMFGQNDQDTHLHWKYDIYEQTKETDSVVLLEN 420
DB 361 VLLLYLKLRLKIIIFPPIDPGKIFKEMFGQNDQDTHLHWKYDIYEQTKETDSVVLLEN 420
QY 421 LKASQ 426
DB 421 LKASQ 426
RESULT 2
AAW24973
ID AAW24973 standard; protein; 427 AA.
XX AC AAW24973;
XX DT 22-JUN-1998 (first entry)
XX

DE Human interleukin-13 alpha receptor.
XX KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
XX OS Homo sapiens.
XX PN WO9720926-A1.
XX PD 12-JUN-1997.
XX PF 07-NOV-1996; 96WO-FR001756.
XX PR 06-DEC-1995; 95FR-00014424.
XX PA (SNFI) SANOFI SA.
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX WPI; 1997-319773/29.
XX DR N-PSDB; AAT85827.
XX PT New purified human interleukin-13 receptors - and related nucleic acids,
XX FT useful for diagnosis and treatment of inflammation, allergy, etc.
XX PS Claim 8; Page 46-47; 83pp; French.
XX CC This sequence represents interleukin-13 (IL-13) alpha receptor. The
XX CC invention relates to new purified peptides comprising 380 or 427 amino
XX CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
XX CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
XX CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
XX CC affinity, but acquires high affinity when associated with the IL-4
XX CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
XX CC diagnostic probes to identify aberrant synthesis or genetic anomalies
XX CC such as loss of heterozygosity and rearrangements, or chromosomal
XX CC anomalies. They are also used for production of recombinant IL-13R beta
XX CC and alpha which can be used as IL-13 antagonists, specifically to
XX CC regulate IL-13-induced responses for treatment of inflammation and
XX CC allergy. IL-13 receptors are also useful as antisense molecules for gene
XX CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
XX CC immunoassays) to diagnose diseases associated with abnormal expression of
XX CC IL-13 receptors; when coupled to a toxin also for treatment of
XX CC overproduction of IL-13R. Cells that express IL-13R at the surface are
XX CC used to identify ligands and modulators of IL-13R
XX SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGGGAAPTETPPVTNLSVSVENLCTVIWTNPPGASSN 59
DB 1 MEWPARGLWALLLCAGGGGGGGAAPTETPPVTNLSVSVENLCTVIWTNPPGASSN 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 119
DB 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 120
QY 120 PEGDPESAATELCIWHNLSYMKCSWLPGRNTSPDTNLTYYWHRSLKIHQCEINFREG 179
DB 121 PEGDPESAATELCIWHNLSYMKCSWLPGRNTSPDTNLTYYWHRSLKIHQCEINFREG 180
QY 180 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSEFNIVPLTSRVKPDPPHINKLSFHND 239
DB 181 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSEFNIVPLTSRVKPDPPHINKLSFHND 240
QY 240 DLYVQWENPQNFISRCIFYEVEVNNSTQETHNVFYVQAEKCNPEPERNVENTSCFMVPG 299
DB 241 DLYVQWENPQNFISRCIFYEVEVNNSTQETHNVFYVQAEKCNPEPERNVENTSCFMVPG 300
QY 300 GVLPTLNTVRIKVTNKLKCYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 359
DB 300 GVLPTLNTVRIKVTNKLKCYEDDKLWSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 359

Db 301 GVLPDTLNTVIRVKTNKLCEYDDKLSNWSQEMSIGKGRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLYLKRLKIIIFPPIDPDKIFKEMFGQNDTLHWKKYDIYEKQTEETDSVVLIE 419
Db 361 IVLLYLKRLKIIIFPPIDPDKIFKEMFGQNDTLHWKKYDIYEKQTEETDSVVLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427

RESULT 3
AAB19807
ID AAB19807 standard; protein; 427 AA.
AC AAB19807;
XX DT 05-MAR-2001 (first entry)
XX Human interleukin-13 receptor alpha-1.
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Sig_peptide
FT Domain 27..347
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Peptide 327..331
FT /note= "WSXWS motif conserved in the type-I cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 368..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXQ motif, consensus for STAT binding"
XX US6143871-A.
XX PN 07-NOV-2000.
XX PD 12-NOV-1997; 97US-00969125.
XX PF 13-DEC-1996; 96GB-00025899.
XX PR (GAUC/) GAUCHAT J.
XX PA (BONN/) BONNEFOY J.
XX XX Gauchat J, Bonnefoy J;
PI WPI; 2001-006445/01.
DR N-PSDB; AAA88907.
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.
XX Claim 2; Fig 1A; 26pp; English.
XX The present sequence is that of a protein capable of binding human
CC interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
CC of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
CC from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
CC polypeptide can be used to inhibit IL-13 or IL-4 induced Ige synthesis in
CC B cells, useful in the treatment of diseases in which Ige or Th2
CC differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,

CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC them which have been shed from cells as a result of disease, e.g. cancer,
CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC syndrome and toxoplasmosis
XX SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MEWPARLCGLWALLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MEWPARLCGLWALLCAGGGGGGAAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWYFHFHFGDKQDKKIAPETRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCIISP 119
Db 61 NCSLWYFHFHFGDKQDKKIAPETRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCIISP 120
Qy 120 PEGDPESAATELOCIWHNLSYMKCSWLPGRNTSPDTNYTLYWHSLEKIHQECENIFREG 179
Db 121 PEGDPESAATELOCIWHNLSYMKCSWLPGRNTSPDTNYTLYWHSLEKIHQECENIFREG 180
Qy 180 QYFGCSFDLTAKVDSSFEQHSVQIMVKNAGIKPSFNIVPLTSRVKPDPPHINKLSFNH 239
Db 181 QYFGCSFDLTAKVDSSFEQHSVQIMVKNAGIKPSFNIVPLTSRVKPDPPHINKLSFNH 240
Qy 240 DDLYVQWENPQNFISRCILFYEVEVNSQTEHNFYVQEAECENPEFERNVENTSCFWVP 299
Db 241 DDLYVQWENPQNFISRCILFYEVEVNSQTEHNFYVQEAECENPEFERNVENTSCFWVP 300
Qy 300 GVLPDTLNTVIRVKTNKLCEYDDKLSNWSQEMSIGKGRNSTLYITMLLIVPVIVAGAI 359
Db 301 GVLPDTLNTVIRVKTNKLCEYDDKLSNWSQEMSIGKGRNSTLYITMLLIVPVIVAGAI 360
Qy 360 IVLLYLKRLKIIIFPPIDPDKIFKEMFGQNDTLHWKKYDIYEKQTEETDSVVLIE 419
Db 361 IVLLYLKRLKIIIFPPIDPDKIFKEMFGQNDTLHWKKYDIYEKQTEETDSVVLIE 420
Qy 420 NLKXASQ 426
Db 421 NLKXASQ 427
RESULT 4
ADL71812
ID ADL71812 standard; protein; 427 AA.
XX AC ADL71812;
XX DT 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) protein.
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..427
FT /note= "Human mature IL-13 R protein"
FT Domain 27..347
FT /note = Extracellular domain
FT Domain 327..331
FT /note = WSXWS motif
FT Domain 368..427

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FT XX /note = Cytoplasmic domain
PN XX
XX US2004043921-A1.
XX 04-MAR-2004.
XX
XX 29-SEP-2003; 2003US-00671697.
XX
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX
XX Bonnefoy J, Gauchat J;
XX
XX WPI; 2004-225726/21.
XX N-PSDB; ADL71811.
XX
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX Claim 1; SEQ ID NO 9; 27pp; English.
XX
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) protein.
XX
XX Sequence 427 AA;
XX
XX Query Match 99.5%; Score 2309.5; DB 8; Length 427;
XX Best Local Similarity 99.8%; Pred. No. 4.4e-211;
XX Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 MWPRLCGIWMALLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
DB 1 MWPRLCGIWMALLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFQDKQKKIAPETRRSIEVPLNERICLVQVGSQCSTNSEKPSILVERCISP 119
DB 61 NCSLWYFSHFQDKQKKIAPETRRSIEVPLNERICLVQVGSQCSTNSEKPSILVERCISP 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCNIFREG 179
DB 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCNIFREG 180
QY 180 QYFGCSFDLTQVDSFEQHSQVIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFN 239
DB 181 QYFGCSFDLTQVDSFEQHSQVIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFN 240
QY 240 DDLYVQWENPQNFISRCLEFVEVNNSTQETHNVFVYQAEKCNPFERNVENTSCFMVP 299
DB 241 DDLYVQWENPQNFISRCLEFVEVNNSTQETHNVFVYQAEKCNPFERNVENTSCFMVP 300
QY 300 GVLPDILTNTVIRVKNKLCYEDDDKLWSNWSQMSIGKKRNSTLYITMLLIVPVIIVAGAI 359
DB 301 GVLPDILTNTVIRVKNKLCYEDDDKLWSNWSQMSIGKKRNSTLYITMLLIVPVIIVAGAI 360
QY 360 IVLLLYLKRLLIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEKEDSVLLIE 419
DB 361 IVLLLYLKRLLIIFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQTEKEDSVLLIE 420
QY 420 NLKKAQ 426
DB 421 NLKKAQ 427

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RESULT 5
ADL82843
ID ADL82843 standard; protein; 427 AA.
XX
XX ADL82843;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human PRO2537, SEQ ID 45.
XX
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
XX Gene Therapy; PRO; B cell related disorder; cancer;
XX Immune-mediated inflammatory disease; human.
XX
XX Homo sapiens.
XX
XX WO2004024097-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029097.
XX
XX 16-SEP-2002; 2002US-0411392P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX Wu TD;
XX
XX WPI; 2004-329389/30.
XX N-PSDB; ADL82842.
XX
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX Claim 10; Fig 45; 695pp; English.
XX
XX The present invention relates to PRO proteins and their coding sequences.
XX The PRO proteins are useful for diagnosing and treating a B cell related
XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX antigen unresponsiveness, selective IGA deficiency, selective IGM
XX deficiency, selective deficiency of IGG subclasses, immunodeficiency with
XX hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX medicament for treating a condition that is responsive to the PRO
XX protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX coding sequences are useful as hybridization probes in chromosome and
XX gene mapping, in preparing PRO proteins, or in generating transgenic
XX animals or knockout animals, which in turn are useful in the development
XX and screening of therapeutically useful reagents.
XX
XX Sequence 427 AA;

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Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MWPRLCGIWMALLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
DB 1 MWPRLCGIWMALLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFQDKQKKIAPETRRSIEVPLNERICLVQVGSQCSTNSEKPSILVERCISP 119
DB 61 NCSLWYFSHFQDKQKKIAPETRRSIEVPLNERICLVQVGSQCSTNSEKPSILVERCISP 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHQCNIFREG 179

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Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCNIFREG 180
Qy 180 QYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQENPQNFISRCCLFYEVVNNSTQTHNVFYVQEAACENPEPERNVENTSCFMVP 299
Db 241 DDLYVQENPQNFISRCCLFYEVVNNSTQTHNVFYVQEAACENPEPERNVENTSCFMVP 300
Qy 300 GVLPTDLTNTVIRVKTNKLKYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 359
Db 301 GVLPTDLTNTVIRVKTNKLKYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
Qy 360 IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE 420
Qy 420 NLKKASQ 426
Db 421 NLKKASQ 427

RESULT 6
ADN04504
ID ADN04504 standard; protein; 427 AA.
AC ADN04504;
XX
DT 01-JUL-2004 (first entry)
DE Antipsoriatic protein sequence #445.
KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
FN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-305105/28.
DR N-PSDB; ADN04503.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 898; 3069pp; English.
PS
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MEMPARGCLGALLCAGGGGGGGAAPTETQPPVTNLSVSNLCTVIWTPNPEGASS 59

Db 1 MEMPARGCLGALLCAGGGGGGGAAPTETQPPVTNLSVSNLCTVIWTPNPEGASS 60
Qy 60 NCSLWYFSGDKODKKIAPETRSTEVPLNERICLVQSGCSTNESEKPSILVEKICSP 119
Db 61 NCSLWYFSGDKODKKIAPETRSTEVPLNERICLVQSGCSTNESEKPSILVEKICSP 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCNIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTYWHSLEKIHQCNIFREG 180
Qy 180 QYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQENPQNFISRCCLFYEVVNNSTQTHNVFYVQEAACENPEPERNVENTSCFMVP 299
Db 241 DDLYVQENPQNFISRCCLFYEVVNNSTQTHNVFYVQEAACENPEPERNVENTSCFMVP 300
Qy 300 GVLPTDLTNTVIRVKTNKLKYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 359
Db 301 GVLPTDLTNTVIRVKTNKLKYEDDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIAGAI 360
Qy 360 IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE 419
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGQNDTTLHWKKYDIYEKQTEETDSVLLIE 420
Qy 420 NLKKASQ 426
Db 421 NLKKASQ 427

RESULT 7
ADN62575
ID ADN62575 standard; protein; 427 AA.
XX
AC ADN62575;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human interleukin 13 (IL-13) receptor alpha 1 chain.
XX
KW Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;
KW IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW cancer; inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
KW Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
KW Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
KW Lyme disease; tuberculosis; malaria; leishmaniasis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..26
FT Protein /note= "Signal peptide"
FT 27..427 /note= "Mature protein claimed in claim 1"
XX
XX US6743604-B1.
XX
XX 01-JUN-2004.
XX
XX 06-APR-2000; 2000US-00545002.
XX
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-409324/38.
DR

DR N-PSDB; ADN62574.
XX
PT New isolated nucleic acid molecule encoding a polypeptide capable of
binding human IL-13 and/or binding human IL-4, useful in medicine, in
PT diagnostics or for producing antibodies.
XX
PT
PS
PS Claim 1; SEQ ID NO 9; 24pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (ADN62574),
CC which encodes the mature form of a polypeptide capable of binding human
CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
CC IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
CC a vector comprising the nucleic acid molecule and a host cell comprising
CC the vector. The nucleic acids are useful as probes or primers or in the
CC analysis of allelic variation. The polypeptides are useful for binding
CC human IL-13 and/or binding human IL-4 and act as inhibitors by
CC interfering with the interaction between human IL-13 or IL-4 and their
CC natural receptors. They can also be used in medicine, e.g. for treatment
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC used for producing antibodies, which can be used for diagnosing diseases.
CC The present sequence represents IL-13 receptor alpha 1 subunit.
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLVSVENLCTVIWNNPPGASS 59
DB 1 MEWPARGLWALLLCAGGGGGGAAPTETQPPVTNLVSVENLCTVIWNNPPGASS 60
QY 60 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNSEKPSILVEKICSP 119
DB 61 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNSEKPSILVEKICSP 120
QY 120 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCNIFREG 179
DB 121 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCNIFREG 180
QY 180 QYFGCSFDLTQVDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 239
DB 181 QYFGCSFDLTQVDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
QY 240 DDLVYQWENPQNIFSRCLFYEVRVNSQTEHNVFVQEAACNPFERNVENTSCFMPV 299
DB 241 DDLVYQWENPQNIFSRCLFYEVRVNSQTEHNVFVQEAACNPFERNVENTSCFMPV 300
QY 300 GVLPLDTLTVIRVTKNLCYEDDKLWSNWSQMSIGKKENSTLYITMLLIVPVIIVAGAI 359
DB 301 GVLPLDTLTVIRVTKNLCYEDDKLWSNWSQMSIGKKENSTLYITMLLIVPVIIVAGAI 360
QY 360 IVLLLYLKRLLKIIFFPIPPDGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 419
DB 361 IVLLLYLKRLLKIIFFPIPPDGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 420
QY 420 NLKKAQ 426
DB 421 NLKKAQ 427
RESULT 8
ABM82441
ID ABM82441 standard; protein; 427 AA.
XX
AC ABM82441;
XX

DT 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
DE
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
OS Homo sapiens.
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
DR N-PSDB; ACN41073.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
PS
PS Claim 12; SEQ ID NO 6271; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 427 AA;
Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.4e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLVSVENLCTVIWNNPPGASS 59
DB 1 MEWPARGLWALLLCAGGGGGGAAPTETQPPVTNLVSVENLCTVIWNNPPGASS 60
QY 60 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNSEKPSILVEKICSP 119
DB 61 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSGCSTNSEKPSILVEKICSP 120
QY 120 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCNIFREG 179
DB 121 PEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSPDNTYLYWHRSLKIHQCNIFREG 179
XX

XX PI Dunlop FM, Baca M, Nash AD, Fabri LJ;
XX WPI; 2003-876912/81.
DR N-PSDB; ADF17834.
XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
PT inflammatory disorder.
XX Disclosure; SEQ ID NO 4; 99pp; English.
XX
XX This invention relates to a novel antibodies that function as interleukin
CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
CC for treating certain conditions induced by IL-13. Specifically, it refers
CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
CC and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
CC system, such that it is involved in the induction of IgE, IgG4 and T-
CC helper cells and accordingly is implicated in conditions from anaphylaxis
CC to hay fever and asthma. As such, the present invention describes these
CC novel antibodies as antiinflammatory, cytostatic, antiulcer,
CC dermatological, antiallergic and antiasthmatic. The methods and
CC compositions are useful for treating various disorders including
CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
CC rhinitis, oncological conditions and chronic obstructive pulmonary
CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
CC protein of the invention.
XX
XX Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 7; Length 427;
Best Local Similarity 99.5%; Pred. No. 2.1e-210;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MEWPRLCGLWALLLCAGGGGGGGG-APTPTQPPVTLNLSVSVENLCTVIWTPNPEGASS 59
DB 1 MEWPRLCGLWALLLCAGGGGGGGGAAAPTQPPVTLNLSVSVENLCTVIWTPNPEGASS 60
QY 60 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 119
DB 61 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 179
DB 121 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 180
QY 180 QYFGCSFDLTAKVSDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 239
DB 181 QYFGCSFDLTAKVSDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 240
QY 240 DDLYVQWENQNFISRCCLFYEVVNNSTQTHNVFVYQEAECENPEPERNVENTSCFMPV 299
DB 241 DDLYVQWENQNFISRCCLFYEVVNNSTQTHNVFVYQEAECENPEPERNVENTSCFMPV 300
QY 300 GVLPDTLNTRVIRVKTNKLCEYEDDKLWSNNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 359
DB 301 GVLPDTLNTRVIRVKTNKLCEYEDDKLWSNNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 360
QY 360 IVLLLYLKRLLKIIFFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEQTKTEEDTSVVLIE 419
DB 361 IVLLLYLKRLLKIIFFPPIPDGKIFKEMFGDQNDTLHWKKYDIYEQTKTEEDTSVVLIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427

RESULT 11
ADL71814
ID ADL71814 standard; protein; 427 AA.
XX
XX AC ADL71814;

XX DT 20-MAY-2004 (first entry)
XX DE Human interleukin-13 receptor alpha (IL-13 Ralpa) mutant, G358D.
XX KW Human, IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
KW mucin.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT Misc-difference 358 /note= "Wild-type Gly is substituted with Asp"
XX US2004043921-A1.
XX PD 04-MAR-2004.
XX XX 29-SEP-2003; 2003US-00671697.
XX PF 13-DEC-1996; 96GB-00025899.
XX PR 12-NOV-1997; 97US-00969125.
XX PR 06-APR-2000; 2000US-00545002.
XX XX (BONN/) BONNEFOY J.
XX PA (GAUC/) GAUCHAT J.
XX PI Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX Claim 14; Page; 27pp; English.
XX The invention relates to polypeptides capable of binding human
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpa. The
CC invention also relates to a method of treatment of a disease in which
CC IL13 and IL4 cause adverse effects. The method is useful for treating a
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
CC of the invention are useful in raising antibodies. It is also useful in
CC gene therapy. The present sequence is human interleukin-13 receptor alpha
CC (IL-13 Ralpa) mutant protein. Note: This sequence is not shown in the
CC specification, however it is constructed based on human IL-13 Ralpa
CC protein shown as SEQ ID NO:9 in the specification.
XX
XX Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 8; Length 427;
Best Local Similarity 99.5%; Pred. No. 2.1e-210;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MEWPRLCGLWALLLCAGGGGGGGG-APTPTQPPVTLNLSVSVENLCTVIWTPNPEGASS 59
DB 1 MEWPRLCGLWALLLCAGGGGGGGGAAAPTQPPVTLNLSVSVENLCTVIWTPNPEGASS 60
QY 60 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 119
DB 61 NCSLWYFHFSGDKQDKKIAPIETRRSIEVPLNERICLVQSGQCSNTESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 179
DB 121 PEGDPESAVTELOCIVHNLNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 180
QY 180 QYFGCSFDLTAKVSDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 239
DB 181 QYFGCSFDLTAKVSDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHKNLSFHN 240

QY 240 DDLYVQWENPNQFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
DB 241 DDLYVQWENPNQFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIIVPVIVAGAI 359
DB 301 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIIVPVIVADAI 360
QY 360 IVLLLYLRLKLIIPFPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKOTKEETDSVVLIE 419
DB 361 IVLLLYLRLKLIIPFPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKOTKEETDSVVLIE 420
QY 420 NLKQASQ 426
DB 421 NLKQASQ 427

RESULT 12

AAB19808
ID AAB19808 standard; protein; 427 AA.

XX AAB19808;

DT 05-MAR-2001 (first entry)

XX Human interleukin-13 receptor alpha-1 variant.

XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Sig_peptide
FT Domain 27..347
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Misc-difference 130
FT /note= "Gly in "
FT Peptide 327..331
FT /note= "WSXHS motif conserved in the type-I cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 368..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXXQ motif, consensus for STAT binding"

XX US6143871-A.

XX 07-NOV-2000.

XX 12-NOV-1997; 97US-00969125.

XX 13-DEC-1996; 96GB-00025899.

XX (GAUC/) GAUCHAT J.
PA (BONN/) BONNEFOY J.

XX Gauchat J, Bonnefoy J;

XX WPI; 2001-006445/01.

XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
FT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.

XX Claim 4; -: 26pp; English.

CC The present sequence is that of a claimed isolated polypeptide which is
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
CC 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a
CC sequence (see AAB19807) deduced from isolated cDNA by having residue 130
CC as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13
CC receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4
CC induced IgG synthesis in B cells, useful in the treatment of diseases in
CC which IgE or Th2 differentiation plays a role, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised
CC against the polypeptide are useful for detecting IL-13 and IL-4 receptor
CC or parts of them which have been shed from cells as a result of disease,
CC e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis,
CC eczema, asthma, lupus erythematosus, AIDS, thyroiditis, diabetes,
CC uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
CC inflammatory bowel disease, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome and toxoplasmosis. Note: The present
CC sequence is not shown in the specification but is derived from the IL-13
CC receptor alpha 1 sequence given in figure 1 (see AAB19807)

XX SQ Sequence 427 AA;

Query Match 99.0%; Score 2296.5; DB 4; Length 427;

Best Local Similarity 99.3%; Pred. No. 7.7e-210;

Matches 424; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MEWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSNELCTVIWTNPPGASS 59

DB 1 MEWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSNELCTVIWTNPPGASS 60

QY 60 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 119

DB 61 NCSLWYFSGDKQDKKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 120

QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 179

DB 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 180

QY 180 QYFGCSFDLTVKQSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRKVDPDPHKNLSFN 239

DB 181 QYFGCSFDLTVKQSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRKVDPDPHKNLSFN 240

QY 240 DDLYVQWENPNQFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299

DB 241 DDLYVQWENPNQFISRCFLFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300

QY 300 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIIVPVIVAGAI 359

DB 301 GVLPTLTNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIIVPVIVADAI 360

QY 360 IVLLLYLRLKLIIPFPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKOTKEETDSVVLIE 419

DB 361 IVLLLYLRLKLIIPFPIDPGKIFKEMFGDQNDTTLHWKKYDIYEKOTKEETDSVVLIE 420

QY 420 NLKQASQ 426

DB 421 NLKQASQ 427

RESULT 13

ADX97531

ID ADX97531 standard; protein; 414 AA.

XX AC ADX97531;

XX 21-APR-2005 (first entry)

XX Pancreatic cancer associated human protein, SEQ ID 79.

XX pancreas tumor; cytostatic.

XX OS Homo sapiens.

XX EP1471075-A2.

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XX PD 27-OCT-2004.
XX PF 31-MAR-2004; 2004EP-00090124.
XX PR 31-MAR-2003; 2003DE-01015834.
XX (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemmendorf T;
PI Lichtner R, Staub E, Roepcke S, Li X;
XX WPI; 2004-768082/76.
DR N-PSDB; ADX97460.
XX New nucleic acid differentially expressed in pancreatic tumor tissue, for
PT use as diagnostic agents and in screening for therapeutic agents.
XX Claim 2; SEQ ID NO 79; 28pp; German.
XX The invention relates to a novel human nucleic acid sequence of the
CC pancreas and its encoded protein. The invention further comprises:
CC proteins and peptides, preferably isolated, that contain a sequence
CC encoded by the novel nucleic acid; and methods for diagnosis and
CC treatment of pancreatic cancer, using a substance that inhibits or binds
CC to the protein or its DNA, including: an antisense oligonucleotide, short
CC interfering RNA or ribozyme directed against the pancreatic protein, an
CC organic molecule, particularly having a molecular weight below 5000,
CC especially 300, that binds to the pancreatic DNA, an aptamer or
CC (monoclonal) antibody, preferably human or humanized, that binds to the
CC pancreatic DNA, or an anti-idiotypic antibody raised against the
CC monoclonal antibody, any of which may be derivatized with a reporter
CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
CC human pancreatic proteins and their encoding DNA have cytostatic
CC activity. The novel sequences are useful for inhibiting transcription
CC and/or expression of genes and proteins associated with pancreatic
CC cancer. This sequence represents one of the novel human pancreatic
CC proteins of the invention. Note: This sequence is not shown in the
CC specification, it has been electronically downloaded from a DVD-ROM
CC provided with this specification by the European Patent Office.
XX SQ Sequence 414 AA;
Query Match 96.1%; Score 2230.5; DB 8; Length 414;
Best Local Similarity 99.8%; Pred. No. 1.5e-203;
Matches 413; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 14 LLCAGGGGGGGG-APTETQPPVTNLSVSNLCTVIWTPNPPGASNCSLWYFSHFGDK 72
DB 1 LLCAGGGGGGGGAAPTETQPPVTNLSVSNLCTVIWTPNPPGASNCSLWYFSHFGDK 60
QY 73 QDKKIAPETRHSIEVPLNERICLVQVGCSTNESEKPSILVEKICISPPGDPESAVTELQ 132
DB 61 QDKKIAPETRHSIEVPLNERICLVQVGCSTNESEKPSILVEKICISPPGDPESAVTELQ 120
QY 133 CIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHQCENTIFREQYFGCSFDLTQVK 192
DB 121 CIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHQCENTIFREQYFGCSFDLTQVK 180
QY 193 DSSFEQHSVQIMVKDNAGKIKPSNIVPLTSRVKPDPPHINKLSFHNDLLYVQWENPQN 252
DB 181 DSSFEQHSVQIMVKDNAGKIKPSNIVPLTSRVKPDPPHINKLSFHNDLLYVQWENPQN 240
QY 253 ISRCLFYEVEVNNNSQTETHNVFYVQAEKCNPFERNVENTSCFMVPGVLPDLTINTVIR 312
DB 241 ISRCLFYEVEVNNNSQTETHNVFYVQAEKCNPFERNVENTSCFMVPGVLPDLTINTVIR 300
QY 313 VTKNLCYEDDKLWSNWSQEMSGKGRNSTLYITMLLIIVPVIAGAILVLLLLKRLKII 372
Db 301 VTKNLCYEDDKLWSNWSQEMSGKGRNSTLYITMLLIIVPVIAGAILVLLLLKRLKII 360
QY 373 IFPPIPDPGKIFKEMFGDQNDTLHWKKYDIYKQTKETSDSVVLIENTLKASQ 426
Db 361 IFPPIPDPGKIFKEMFGDQNDTLHWKKYDIYKQTKETSDSVVLIENTLKASQ 414
RESULT 14
AAU69132
ID AAU69132 standard; protein; 405 AA.
XX AC AAU69132;
XX 29-JAN-2002 (first entry)
XX Canine interleukin 13 receptor PcaIL-13Ralpha1 405.
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IL-13Ralpha2; immunoglobulin heavy chain; I9G Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX Canis familiaris.
XX W0200177332-A2.
XX 18-OCT-2001.
XX 09-APR-2001; 2001WO-US011498.
XX 07-APR-2000; 2000US-0195659P.
PR 07-APR-2000; 2000US-0195874P.
XX (HESK-) HESKA CORP.
XX McCall CA, Tang L;
PI WPI; 2001-657172/75.
DR N-PSDB; AAS59954, AAS59956.
XX Novel isolated canine protein, preferably canine immunoglobulin G protein
PT or canine interleukin-13 receptor protein useful for regulating immune
PT response of an animal and for developing regulatory compounds.
XX Claim 18; Page 164-165; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor
CC protein, the nucleic acids encoding them, antibodies raised against them,
CC fusion proteins between the IgG and IL-13R proteins and methods of
CC isolating regulators of them. The regulators are useful for regulating an
CC immune response in a canine. The regulators are useful to develop regulatory
CC compounds including inhibitors and activators that, when administered to
CC a canine in an effective manner, are capable of protecting canine from
CC disease mediated by IL-13Ralpha or IL-13. The regulators are useful for
CC treating canine IgG (heavy and/or light chain) and/or canine IL-13R
CC mediated responses. The molecules of the invention are useful to regulate
CC the immune response of an animal (e.g. by gene therapy). The present
CC sequence represents a protein of the invention
XX SQ Sequence 405 AA;
Query Match 80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 6.1e-170;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;
QY 22 GGGGAPETQPPVTNLSVSNLCTVIWTPNPPGASNCSLWYFSHFGDKQDKKIAPET 81
DB 1 GGVAAPETQPPVTNLSVSNLCTVIWTPNPPGASPNCTLRYFSHFDNKQDKKIAPET 60
QY 82 RRSIEVPLNERICLVQVGCSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSY 141
```

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Db 61 HRSKEVPLNERICLQVGSQSTNESDNPISLVEKCTPPPEGDPSAVTELQCVWHNLSYM 120
Qy 142 KCSWLPNGHTSPDNTYLYYHRSLEKIHQENIFREGQYFGCSFDLTKKVQSSFEQHSV 201
Db 121 KCTLWPGHTSPDNTYLYYHSSLGKTLQCEDIYREGQHTGCSFALTNLKDSSFEQHSV 180
Qy 202 QIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDIYVQWENPQNFIISCLFVEV 261
Db 181 QIMVKDNARKLRPSFNIVPLTSRVKPDPPHINKLRFQNGNLYVQWKPNQPNFYSRCLSQV 240
Qy 262 EVNNSQTETHNVFYVQEAECENPFERNVENTSCFMVPGVLPDITLNTVIRVTKNKLCYE 321
Db 241 EVNNSQTETNDIFVYVEAKQNSPEEGNLEGTICFMVPGVLPDITLNTVIRVTKNKLCYE 300
Qy 322 DDKLSWNSQNSIGKNSLYITMLIVVIVAGAIIVLLVYKRLKIIIFPPIDPG 381
Db 301 DDKLSWNSQNSIGKNSLYITMLIVVIVAGAIIVLLVYKRLKIIIFPPIDPG 360
Qy 382 KIFKEMFGDQNDTLHWKXYDIYEKQTEEDTSVVLLENLKKASQ 426
Db 361 KIFKEMFGDQNDTLHWKXYDIYEKQTEEDTSVVLLENLKKASQ 405
```

```
RESULT 15
AA92208
ID AA92208 standard; protein; 793 AA.
XX
AC AA92208;
XX
DT 01-AUG-2000 (first entry)
XX
DE IL-13/IL-4 dual trap, IL-13-R-alpha-1, IL-4-R-alpha-Pc fusion protein.
XX
KW IL-13/IL-4 dual trap; cytokine; antagonist; CNTF; receptor;
XX fusion protein; cytostatic; immunomodulator; osteopathic.
XX
OS Synthetic;
XX Homo sapiens.
XX
FH Key
FT Protein 1.343
FT /label= human IL-13-R-alpha-1
FT /note= "extraCellular domain"
FT Protein 254..564
FT /label= IL-4-R-alpha
FT /note= "extracellular domain"
FT Peptide 344..353
FT /label= linker
FT Peptide 565..566
FT /label= linker
FT Protein 567..793
FT /label= human_Pc
XX
PN WO200018932-A2.
XX
PD 06-APR-2000.
XX
PF 22-SEP-1999; 99WO-US022045.
XX
PR 25-SEP-1998; 98US-0101858P.
XX 19-MAY-1999; 99US-00313942.
XX (REG-) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX
XX WPI; 2000-293165/25.
XX N-PSDB; AAA09050.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases or
XX disorders encodes a fusion polypeptide capable of binding a cytokine to
XX form a nonfunctional complex.
```

```
PS This sequence shows an IL-13/IL-4 single chain dual trap fusion protein,
XX designated IL-13-R-alpha-1, IL-4-R-alpha. The invention concerns
XX production of antagonists to any cytokine that utilizes an alpha
XX specificity determining component, which when combined with the cytokine,
XX binds to a first beta signal transducing component to form a non-
XX functional intermediate which then binds to a second beta signal
XX transducing component causing beta-receptor dimerization, the soluble
XX alpha specificity determining component of the receptor (sR-alpha) and
XX the extracellular domain of the first beta signal transducing component
XX of the cytokine receptor (beta-1) are combined to form heterodimers (sR-
XX alpha:beta-1) that act as antagonist to the cytokine by binding the
XX cytokine to form a non-functional complex. The receptor components are
XX shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
XX of cytokines. The invention provides the basis for the development of IL-
XX 6 antagonists, as they show that if, in the presence of a ligand, a non-
XX functional intermediate complex, consisting of the ligand, its alpha
XX receptor and its beta-1 receptor component, can be formed, it will
XX effectively block the action of the ligand. Effective antagonists of IL-6
XX or CNTF consist of heterodimers of the extracellular domains of the alpha
XX specificity determining components of their receptors and the
XX extracellular domain of gpl30. The resultant heterodimers, function as
XX high-affinity traps, rendering the cytokine inaccessible to form a signal
XX transducing complex with the native membrane-bound forms of their
XX receptor. The nucleic acids and polypeptides are useful for treating
XX cytokine-related diseases or disorders such as osteoporosis and primary
XX and secondary effects of cancer including multiple myeloma or cachexia
XX
XX Sequence 793 AA;
XX
XX Query Match 80.8%; Score 1875.5; DB 3; Length 793;
XX Best Local Similarity 99.4%; Pred. No. 2.8e-169;
XX Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MWPRLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPPEGASS 59
Db 1 MWPRLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVITWNPPEGASS 60
Qy 60 NCSLWYFSHFCDKQDKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVKECISP 119
Db 61 NCSLWYFSHFCDKQDKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVKECISP 120
Qy 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTQVQSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDDPPHINKLSFN 239
Db 181 QYFGCSFDLTQVQSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDDPPHINKLSFN 240
Qy 240 DDLYVQWENPQNFIISCLFYEVEVNNSTETHNVFYVQEAECENPFERNVENTSCFMV 299
Db 241 DDLYVQWENPQNFIISCLFYEVEVNNSTETHNVFYVQEAECENPFERNVENTSCFMV 300
Qy 300 GVLPDITLNTVIRVTKNKLCYEDDDKLSWNSQNSIGKNS 342
Db 301 GVLPDITLNTVIRVTKNKLCYEDDDKLSWNSQNSIGKNS 343
XX
XX Search completed: February 8, 2006, 21:59:08
XX Job time : 134.105 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 25.2554 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPALCGLWALLCAGGG.....QTKETDSVVLINLKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1653	71.2	426	2 JC7773	IL-13ralpha 1 prot
2	318	13.7	415	2 S12357	interleukin-5 rece
3	294.5	12.7	420	2 S21052	interleukin-5 rece
4	269.5	11.6	348	2 JC7907	common cytokine re
5	229	9.9	335	2 A0267	interleukin-5 rece
6	228	9.8	400	2 S06945	granulocyte-macrop
7	207	8.9	373	2 A55718	interleukin-2 rece
8	205.5	8.9	369	2 I49280	interleukin-2 rece
9	202	8.7	369	2 A42565	interleukin-2 rece
10	197.5	8.5	831	2 J01655	prolactin receptor
11	190	8.2	610	2 A34631	lactogen receptor
12	189	8.1	310	2 A29884	prolactin receptor
13	189	8.1	412	2 A41070	prolactin receptor
14	189	8.1	610	2 A36116	prolactin receptor
15	186	8.0	581	2 I45971	prolactin receptor
16	185	8.0	616	2 A30304	prolactin receptor
17	183	7.9	292	2 I7525	prolactin receptor
18	180	7.8	303	2 I7524	prolactin receptor
19	180	7.8	608	2 I53269	prolactin receptor
20	176	7.6	630	2 I51086	prolactin receptor
21	173	7.5	918	2 A36337	membrane glycoprot
22	172.5	7.4	288	2 B59405	prolactin receptor
23	172.5	7.4	376	2 A59405	prolactin receptor
24	172.5	7.4	622	2 A40144	cytokine receptor
25	170	7.3	897	1 A39255	interleukin-3 rece
26	165	7.1	396	2 I52909	prolactin receptor
27	163	7.0	830	2 I50455	prolactin receptor
28	162.5	7.0	333	2 S13684	granulocyte-macrop
29	161.5	7.0	1092	2 JX0312	differentiation-st

30	157	6.8	378	2 A40266	interleukin-3 rece
31	157	6.8	896	1 A35782	cytokine receptor
32	156.5	6.7	378	2 S50040	granulocyte-macrop
33	154.5	6.7	896	2 I56563	interleukin-3 rece
34	149	6.4	878	1 A40091	interleukin-3 rece
35	146.5	6.3	608	2 S32823	somatotropin recep
36	145	6.2	638	2 A33991	somatotropin recep
37	144.5	6.2	1097	2 S17308	leukemia inhibitor
38	144	6.2	918	2 A44257	interleukin-6 sign
39	142.5	6.1	917	2 I49699	glycoprotein 130 -
40	141	6.1	638	2 S12136	somatotropin recep
41	140	6.0	638	2 E28176	somatotropin recep
42	139	6.0	508	1 ZUHUR	erythropoietin rec
43	139	6.0	634	2 S33339	somatotropin recep
44	135.5	5.8	286	2 S50039	granulocyte-macrop
45	134.5	5.8	557	2 A32694	interferon alpha/b

ALIGNMENTS

RESULT 1

JC7773
IL-13ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7773
R:Pierrrot, C.; Benignel, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell proliferation
C:Genetics:
A:Gene: il-13ralpha

Query Match	71.2%	Score	1653	DB 2	Length	426			
Best Local Similarity	73.3%	Pred. No.	3e-121						
Matches	313	Conservative	43	Mismatches	67	Indels	4	Gaps	3
Qy	1	MEWPALCGLWALLCAGGGGGGAGTETPTPTNLSVSVENLCTVITWNPPEGASSN	60						
Db	1	MARPAWLGELLVLLFFAASLDQVALA-TEVOPPTNLSVSVENLCTVITWNPPEGASPN	59						
Qy	61	CSLWYFSGHFGDKDKKIAPETRRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKICISPP	120						
Db	60	CSLAYFSGHFDQDKKIAPETRRKELPLNEKICLVQSGQCSSTNESEKPSILVKKICISPP	119						
Qy	121	EGDPESAVTELOCTWHLNLSYKCSWLPGRNTSPDNTNLTYYWHSLEKIHOCENIFRSGQ	180						
Db	120	RGSESATVTELOCTWHLNLSYKCSWLPGRNTSPDNTNLTYYWHSLEKIHOCENIFRSGQ	179						
Qy	181	YFGCSFDLTKVKDSSFEHVSQIWMKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHD	240						
Db	180	HIGCSFKLTKV-ESNTEHNIQIWMKNAGKIRPSYKIVSFTSNVKGPPPHIKHFLKNG	238						
Qy	241	DLTYQWENPQNFISRCFLFYEVEVNNSTQETH--NVFYVOEAKCENPEFERNVENTSCFMV	298						
Db	239	ALFVQWKPNQFSSRCLSYEVEVNNSTQETH--NVFYVOEAKCENPEFERNVENTSCFMV	298						
Qy	299	PGVLPDPTLVTRIRVKTNKLCTYEDDKLNSWQESIGKKRNTLYITMLLIVPVIVAGA	358						
Db	299	PGVLNNTVTVRVKTNKLCTYEDDKLNSWQESIGKKRNTLYITMLLIVPVIVAGA	358						
Qy	359	ITVLLYLKRLKIIIFPPIPDGKIFKEMFGQNDTTLHWKKYDIYERQKETSQVLI	418						
Db	359	ITVLLYLKRLKIIIFPPIPDGKIFKEMFGQNDTTLHWKKYDIYERQKETSQVLI	418						
Qy	419	ENLKKAS	425						

Db 419 ENLKAA 425

RESULT 2
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S12357
R:Takaki, S.; Tominaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.
EMBO J. 9, 4367-4374, 1990
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260; PMID:2265612
A:Accession: S12357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: UNIPROT:P21183; UNIPARC:UPI0000028472; GB:D90205; NID:g220465; PIDN:
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.7%; Score 318; DB 2; Length 415;
Best Local Similarity 23.9%; Pred. No. 4.2e-17;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 32 PPVTNLSVSVENICTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRPSIEVPL 89
Db 29 PPV-NFTIKATGLAQVLLHWDPNPQEQRRHVDLEYHVKNAPQEDBYDTRKTESKCVTPL 87

QY 90 NERICLQVGSQCSSTNESEKPSILVERKICISPPGDPESAVTELQCIWHNL----- 138
Db 88 HEGFAASVRLTKSSHTTLASSWVSAELKAPGSPGTSVTLCTHTTVVSSHILRPYQ 147

QY 139 SYMKCSWLPGRNTPPTNTLYYWHRSLEKIHCENIFRE--GQYFGCSFDLTQVKDSSP 196
Db 148 VSLRCTWLVGKADPDTQYFLYRFGVLTE--KCQESYRDALNRNACWFPRTFINSKGF 205

QY 197 EQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQN-FISR 255
Db 206 EQLVHNGSSKRAAIKPFQDLPSLAIDQVNPFRNVTVEIESNLSYIQWEKPLSAPDPH 265

QY 256 CLFYEVEVNSQPTETHNFVYQBAKCNPEFERNVENTSCFMVPGVPLDTLNTVRIRVKT 315
Db 266 CFNYELKIYTKNG-----HIQKEKLIANKISKIDDVSTY-----SIQVRAAV 309

QY 316 NKLCEYEDDKLNSWSEMGISGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKII---- 372
Db 310 SSPCRMPGR-WGEWSQPIYVGERKS-LVEWHILVLP--TAACFVLLIFSLICRVCHLW 364

QY 373 --IFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVV 416
Db 365 TRLFPPVPAPKSNIKDL-----PVVTEYEKPSNETKIEVV 399

RESULT 3
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815; PMID:1732409
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: UNIPROT:Q14633; UNIPARC:UPI00000729BE; EMBL:X61176; NID:g33843; PIDN:
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395,'I' <MU2>
A:Cross-references: UNIPARC:UPI0000179A7F; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID
A:Experimental source: clone lambda h5R.27

A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332,'K' <MU3>
A:Cross-references: UNIPARC:UPI0000179A80; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID
A:Experimental source: clone lambda h5R.25
R:Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verbee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A:Reference number: A46175; MUID:92357767; PMID:1495999
A:Accession: A46175
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Cross-references: UNIPARC:UPI0000179A81
A:Experimental source: HL-60 cells and eosinophils
A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA
A:Residues: 1-128,'I',130-395,'I' <MUW>
A:Cross-references: UNIPARC:UPI000006EDIC; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128,'I',130-332,'K' <MU4>
A:Cross-references: UNIPARC:UPI000006D11E; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F;345-365/Domain: transmembrane #status predicted <TM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 294.5; DB 2; Length 420;
Best Local Similarity 24.8%; Pred. No. 2.9e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 32 PPVTNLSVSVENICTVIWTWNP-PEGASSNCSLWYFSHFQDKQDKKIAPETRPSIEVPLN 90
Db 32 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNLEY-----QVKINAPK-EDDYETRI 82

QY 91 ERICLQV-----GSQCSTNESEKPSILVEKCTIS-----PPEGDPESAVTELQCIWHNL--- 138
Db 83 ESKCVTLHKGFSAVSRVTILQNDHSLSSASAEHLHAPPGSPGTSVNLCTTTNTEDN 142

QY 139 -----SY---MKCSWLPGRNTPPTNTLYYWHRSLEKIHCENIFRE--GQYFGCSFDL 188
Db 143 YSRLRSYQVSLHCTWLVGTDAPDTQYFLYIRYGSWTE--ECQEYSKDTLGRNIACWFP 200

QY 189 TKVQDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 248
Db 201 TILSKGRDLAVLVNGSSKHSARIPFDQLFALHAIQINPLNVTAEIEGTLSIQWEK 260

QY 249 PQN-FISRCLEFYEVEVNSQPTETHNFVYQBAKCNPEFERNVENTSCFMVPGVPLDTLN 307
Db 261 PVSAPFIHCFDEYVKIHNRNG-----YLQIEKLMTNAFISIIDLSKY----- 304

QY 308 TVRIRVKTNKLCEYEDDKLNSWSEMGISGKRNSTLYITMLLIVPVIVAGAIIVLLYLK 367
Db 305 DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIMATIFILILSLICK 363

QY 368 --RLKIIIPPIPDGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVL 417
Db 364 ICHLWIKLFPPIAPKSNIKDLFVITN-----YEKAGSSETELEVI 404

RESULT 4
JC7907
common cytokine receptor gamma chain, isoform a - chicken
C:Species: Gallus gallus (chicken)

C/Accession: JC7907
E/Min, W.: Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A/Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A/Reference number: JC7907; MUID:2325486; PMID:12437989
A/Accession: JC7907
A/Molecule type: mRNA
A/Residues: 1-348 <MIN>
A/Cross-references: UNIPROT:Q8AUP2; UNIPARC:UPI000000P5604; GB:AJ419897; GB:AJ419898
A/Experimental source: e99
C/Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
ment and proliferation.
C/Genetics:
A/Gene: ch gamma-c-a

Best Local Similarity 26.2%; Pred. No. 2e-13;
Matches 85; Conservative 60; Mismatches 125; Indels 55; Gaps 15

db 23 SPSPKG-----VECILNEEYNTCTWGSGTLT--ANYSLYYYWENI.PVVECOQYL 72

73 WDRSVRIGRFEOSFI--IOFOAFVYRVNASCNIGOTLEIPSNRMELONLVKPEAP--VNL 128

db 129 TIHMSGNOLLTWSSPY-KEOCLHVVKYKSNKOTSWTN-----QEVK----- 172

db 173 -GVIFSPSDVDEKYKTYTFYVRSKLNNYC-GNTOLMSEWSVPVFG--NNSTSGKVAEEQL 228

229 0WF6IHTVLIPIASCLLVLVLVLRMERYVWIMPRIPNSKNFDDIFITHNGDFQEW 288

289 VGVPKDVVESFKPNYSIESICHVSEL 313

A40267
interleukin-5 receptor alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C;Accession: A40267
R;Tavernier, J.; Devos, R.; Cornelis, S.; Tuytens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A;Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A;Reference number: A40267; MUID:92005669; PMID:1833065
A;Accession: A40267
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <TAV>
A;Cross-references: UNIPROT:Q01344; UNIPARC:UPI000002ABD4; GB:M75914; NID:g186387; PIDN:
C;Keywords: cytokine receptor; transmembrane protein

Best Local Similarity	24.7%;	Pred. No. 2.8e-10;	
Matches	82.	Conservative	51: Mismatches 147: Indels 52: Gaps 14

32 ppy-net1k7gtlgaovllowknpdpocornwley-----ovknapk- eddyetr1t 82

83 ESKCVTILHKGFASVRTILONDSHLSASSWASAEIHAPPGSGTSIVLTCVTNTTNDN 142

[illegible]

S06945

N;Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: S06945; A1286; A4474
R:Gearing, D. P.; King, J. A.; Gough, N. M.; Nicola, N. A.
EMBO J. 8, 3667-3676, 1989
A:Title: Expression cloning of a receptor for human granulocyte-macrophage colony-
A:Reference number: S06944; MUID:90059866; PMID:255371
A:Accession: S06945
A:Molecule type: mRNA
A:Residues: 1-400 <GEA>
A:Cross-references: UNIPROT:P15509; UNIPARC:UPI0000000C45; EMBL:X17648; NID:g32087
B:Cross-references: Mathev-Prevot, B.; Nathan, D.G.; Sieff, C.A.

A:Reference number: A41286; MUID:91352066; PMID:1715577
A:Accession: A41286
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 347-400 <CRO>
A:Cross-references: UNIPARC:UPI000017C141
R:Rappold, G.; Willison, T.A.; Henke, A.; Gough, N.M.
Genomics 14, 455-461, 1992
A:Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2
A:Reference number: A44474; MUID:93052350; PMID:1358805
A:Accession: A44474
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'N', 377-400 <RAP>
A:Cross-references: UNIPARC:UPI00000723FC; GB:S48539; NID:g258858; PIDN:AAB23942.1; PID:
A:Note: sequence extracted from NCBI backbone (NCBIP:117960)
C:Genetics:

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
 C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor
 F:322-346/Domain: transmembrane #status predicted <TM>
 F:46.54.99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #
 Query Match 9.8% Score 228 DB 2: Length 400;

Best Local Similarity	22.4%; Pred. No. 4.2e-10;		
Matches	90; Conservative	82; Mismatches	180;
		Indels	50; Gaps
			18

29 TVAPASSINVRFDSP-TNLSWDCOENTTFKCEL-----TDKNRVVEPRLSNNESC 81

82 TEREICTEGVTFFEVHNTSORGFOOKLLYPNSGREGTAQNFSCFIYNADLMNCTWARG 141

QY 149 RNTSPDNTYLYYHRSLEKIHOCENIFRE-GQYFGCSFD-LTKVKDSSFEQHSVQIMVK 206
Db 142 PTAPRDVOYFLYIRNSKRREIRCFYIQDSGTHVGCHLONLSGLTSRNT-----FLVN 195
QY 207 DNAGKIKPSF--NIVPLTSRVKPPPHIKNLSFINDLLYYQWENPNF--ISRCLF-YEV 261
Db 196 GTSREIGIQPDSLLDTKIERFNPSPNVTVCNTTCLVWKQPRYQKLSYLDFOYQL 255
QY 262 EVN--NSQTETHNVFFVOEAKCENPEFERNVENTSCFMVPGVLPTDLTNTVIRVKTNKLK 319
Db 256 DVHRKNTQPGTENLLINVSGDLENR-----YNFSPSEPRAKHSVKIRAADVRL 304
QY 320 YEDDKLSNWSQMSIGKKNSS--TLYITMLLIVPVIVAGAIIVLLLYLRLKI-IIFPP 376
Db 305 N-----WSSSEAEFGSDGNLGSVYIYLLIVGTILVCG-IVLGFPLKRFRLIORLFP 358
QY 377 IPDPGKIFKEMFGDON--DDTLHWKYDYIE-KQTEETOSV 415
Db 359 VPQ-----IKKLNNDHVEBEIIWEFTPEGKYREEVLTV 396

RESULT 7
A55718
Interleukin-2 receptor gamma chain precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A55718
R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.P.; Felsburg, R.
Genomic 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
A;Reference number: A55718; MUID:95130114; PMID:7829104
A;Accession: A55718
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P40321; UNIPARC:UPI00000128C41; GB:U04361; NID:G517411; PIDN:
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication

Query Match 8.9%; Score 207; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 1.7e-08;
Matches 76; Conservative 52; Mismatches 131; Indels 44; Gaps 14;

QY 87 VPLNERICLVGSGCSTNESEKLSILVEKICSPGDPESAVTELOCIWNLNLSYMKCSWL 146
Db 21 VGLNSTVPMENG-----NEDITDPFLTATPSETLSVSLPLPEVQCFVFNVEYMNCTWN 75
QY 147 PGRTSPDNTYLYYHRSLE--EKIHOCEN-IFREGQYFCSPDLTKVKDSSFEQHSVQI 203
Db 76 SSSEPRP-TNLTLYHYWYKNSNDKQVQSCGYLFSREVTAGCW--LQKEITHLYETFFVQL 132
QY 204 MVKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN-----DDLXVQWENPNQFISRCLFYE 260
Db 133 --RDPREPRQSTQKQLQNLVLPWAP--ENLILNLSQSLSWSN--RHLDHCLHVV 186
QY 261 VEYVNSQTETHNVFFVOEAKCENPEFERNVENTSCFMVPGVLPTDLTNTVIRVKTNKLKY 320
Db 187 VOYRSDWRDWT-----EQSVDRHNSFLSPSDVQGFYFVRVRSRYNPLCG 232
QY 321 EDDKLSNWSQMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKLKLIIFP 375
Db 233 SAQR--WSEWHPHWSGNTSKENPLFASEAVLPLGSMGLIISLCIYVWLER-----SIP 287
QY 376 PIP 378
Db 288 RIP 290

RESULT 8
I49280
Interleukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)

C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gan
A;Reference number: A47514; MUID:93391374; PMID:8378320
A;Accession: I49280
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <CAO>
A;Cross-references: UNIPROT:P34902; UNIPARC:UPI0000001949; EMBL:U21795; NID:G727349; PIDN:
A;Accession: A47514
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE2>
A;Cross-references: UNIPARC:UPI0000001949; GB:I20048; NID:G404067; PIDN:AAA39286.1; PID:
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of functi
A;Reference number: JN0592; MUID:93277575; PMID:8503926
A;Accession: JN0592
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <KUM>
A;Cross-references: UNIPARC:UPI0000001949; DBJ:DJ3565; NID:G303684; PIDN:BA02760.1; PI
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A;Reference number: JN0775; MUID:93366191; PMID:8359699
A;Accession: JN0775
A;Molecule type: mRNA
A;Residues: 1-369 <KOB>
A;Cross-references: UNIPARC:UPI0000001949; GB:DJ3821; NID:G436045; PIDN:BA02974.1; PID:
R;Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A;Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A;Reference number: S37582
A;Accession: S37582
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-350,'S',352-366,'S',368-369 <CHI>
A;Cross-references: UNIPARC:UPI0000176753; EMBL:X75337
R;DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A;Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal loc
A;Reference number: I53398; MUID:95104285; PMID:7805729
A;Accession: I53398
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <RES>
A;Cross-references: UNIPARC:UPI0000001949; GB:S75852; NID:G861554; PIDN:AAB32904.1; PID:
C;Genetics:
A;Gene: IL-2Rgamma
A;Introns: 39/1, 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C;Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (se
epcors.
C;Function:
A;Description: receptor for interleukin-2
A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F;256-284/Domain: transmembrane #status predicted <TMW>
F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 205.5; DB 2; Length 369;
Best Local Similarity 24.0%; Pred. No. 2.1e-08;
Matches 76; Conservative 63; Mismatches 121; Indels 57; Gaps 16;

QY 102 STNESEKPSILVEKICSPGDPESAVTELOCIWNLNLSYMKCSWLPGRTNTPD---TNYT 158
Db 31 SANEDIKADLLITSTAPEHLISAPLPLPEVQCFVFNVEYMNCTW---NSSSEFQATNLT 86


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QY 159 LYVHRSLEKHQCENTIFREGQYFGCSPLDTKVKDSSPEQHSVQ-----IMVKDNAGKI 212
Db 87 LHRYRYKVSQ-----NNTFQECSHYLFKEIT--SGCQIQKEDIQLYQTFVVLQDPQPKQ 139
QY 213 KPSFNIPLTSRVKPDPPHINKLSFHN---DDLXVQVENPQNFISRLCFYEVEVNNSQTE 269
Db 140 RRAVQKLNQNLVIRAP--ENLTLNLSQESQELRWKS-RHIKERCQLVLQVRSNRDR 196
QY 270 THNVFYVQEAACENPEFERNVENTSCFNVPGVLVPTLN--TVIRVKTNKLCEYEDDKLWS 327
Db 197 SWT-----ELIVNHEPRFSLPSV--DELKRYTFVRKSRYPNCPICGSSQ--WS 239
QY 328 NWSQEMSIGK---KRNSTLYITMLLIVPVIAGAILVLL---YLKRLKILIIFFPIPDG 381
Db 240 KWSQFVHWGSHVTEENPSLFALEAVLIPVGTMGILITLIFVYCWLERM-----PPIP-PI 293
QY 382 KIFKEMFGQDNDTLHW 398
Db 294 KNLDELVTYQGNFSAW 310

RESULT 9
A:Species: Homo sapiens (human)
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42565; A46591; I54332
R:Takeshita, T.; Aseo, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.; Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335983; PMID:1631559
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid, protein
A:Residues: 1-369 <TAK>
A:Cross-references: UNIPROT:P31785; UNIPARC:UPI0000000DEA; GB:D11086; NID:G303611; PIDN:
A:Experimental source: MOLT beta lymphoid cells
A>Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293987; PMID:8514792
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked
A:Reference number: I54332; MUID:94004847; PMID:8401490
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an X-linked form of severe combined immunodeficiency
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 8.7%; Score 202; DB 2; Length 369;
Best Local Similarity 27.2%; Pred. No. 4e-06;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

QY 130 ELQCIWHLNLSYMKCSWLPGRNTSPDNTLYYWHRSLS--EKIHQCEN-IFREGQYFGCSF 186
Db 59 EVQCFFVFNVEYMNCTNWSNSRQP-TNLTLLHWYKNSDNDKVKQKSHYLFSEITSGC-- 115

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QY 187 DLTKVKDSSPEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHINKLSFH---NDDLY 243
Db 116 QLQKKEIHLQYTFVQL--QDPRPRQAQOMLKLQNLVIPWAP--ENLTLHLKLSQLE 171
QY 244 VQVENPQNFISRLC-----FYEVEVNNQTEHNVFYVQEAACENPEFERNVENTSCFNV 299
Db 172 LWNVN--RFLNHCLEHLVQYRTDWDHSWT-----EQSDVYRHKFSLP 211
QY 300 GVLPTDLTVIRVKTNKLCEYEDDKLWSNWSQEMSIG---KRNSTLYITMLLIVPVI 356
Db 212 SVDGQKRYTRFVRSRFNPLC--GSAQHSWSESHPIHWSNTSKENPFLEAVVISVGS 270
QY 357 GAILVLL---LYLKRLLKILIIFFPI 378
Db 271 GLIISLLCVFWLER-----TMRIP 291

RESULT 10
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:G222848; PID
A:Experimental source: kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
Query Match 8.5%; Score 197.5; DB 2; Length 831;
Best Local Similarity 23.1%; Pred. No. 2.6e-07;
Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

QY 31 QP--PVTNLSVSVENLCTV--LWT-WNPP--EGASSNCSLWYFSGHFGDKQDKIAPETRR 83
Db 126 QPGSPV-NLTLETKRANIMYLWAKWSPDLLADASN----HLVYH----ELRIKPEKE 176
QY 84 SIEVPLNERICLQVGSQCSTNE-----SEKPSILVERKCI8PP 120
Db 177 EWET-----ISVGVTQCKINRLNAGMYVQVVRTLPDGEWSEWSSERHILIPSGQSP 231
QY 121 EGDPESAVTELCQIWNHLSYMKCSWLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 180
Db 232 E-----KPTIIKCRSPEKETFTCWKPGLDGCHPTNTYLLYSKEGEQVYECPD-YRTAG 285
QY 191 YFGCSFDTKVKDSSPEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPP-----HIKNL 235
Db 286 PNSCYFD--KKHTSFWTIYNITVRATNEMGNSSDPHYVDVTYIVQPPPVNVTLELKKP 343
QY 236 SFHNDLXVQVENPQNFISR----CLFYEVEVNNQTEHNVFYVQEAACENPEFERNV 291
Db 344 INRKPYLVLTWSPPLPADVRSGWLTLEVLRLKPEGESEWETIFVGQ-QTOYKMSLN-- 400
QY 292 NTSCEFMVGVLPDLTNTVIRVKTNKLCEYEDDKLWSNWSQEMSIGKRNSTLYITMLLIV 351
Db 401 -----PGKVIIOHCKP-----DHGWSWSEWSSSENYIQIPNDFRVKDMIVIV 444
QY 352 PVIVAGAILVLL---LYLKRLLKILIIFF--PPTDP 380
Db 445 LGVLSLLCLIMSWTMTVLKGYRMITFMLPPVPGP 478

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[illegible]

R;Shirot, M.; Barville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J. Mol. Endocrinol. 4, 1136-1143, 1990
A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A:Reference number: A36116; PMID:91155946; PMID:2293022
A:Accession: A36116
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <SH1>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI00000170ADB; GB:M57668; NID:g206366; PIDN:F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.1%; Score 189; DB 2; Length 610;
Best Local Similarity 23.7%; Pred. NO. 8e-07;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

Qy	108	KPSILVBEKCISSPPGDPBSAVTELQCIWHNLVSNKCSWLPGRNTSPDNTIYLYWHRSLE	167
Db	25	KPEI--HKCRSP-----DKET-----FTCWNNPGTDGGLPTNLSLTYSKSGEK	65
Qy	168	KIHOCENIFREGQYFGSGFDLTVKDKSSFEHGSVQIMVKDNAGKIKPSFNIVPLTSLR	227
Db	66	TTYECPDYKTSQPN-SCFP--SKQYTSIWKIYIITVATNATNQMGSSSDPLVVDYTV	122
Qy	228	DPP-----HIKNLSFHNDLLYVOMENPQNFI--SR-----CLFYEVEVNNNSQTETHNVFVQ	278
Db	123	EPPRNLTLVQKQDKKTYLWVKNSPPTITDVKKTGWFTMEYRIKLPKEAEWEIHF---	179
Qy	279	AKCENPFRNVENTSCFMVPGVLPDTLNTRVIRKTNKLCYEDDKLWNSNQSMSIGKK	338
Db	180	-----TGHTQPKFVDFLPGQKYLQTR-----CKPDHGYSWRNSQSSSVEMP	222
Qy	339	RNSTLYITMLLIIVPVIAGAIIVLLIYLLKRLK-----IIIPPPIDPP	380
Db	223	NDPPIKDTTWIIVAILSAVICTLWMAVAALKGYSMMTCIFFPPVPGP	269

RESULT 15

I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-59, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019; PMID:11338725
A:Accession: I45971
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: UNIPROT:Q21872; UNIPARC:UPI0000132230; GB:L02549; NID:g163617; PIDN:
C:Genetics:
A:Gene: PRLR
P:36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.0%; Score 186; DB 2; Length 581;
Best Local Similarity 24.3%; Pred. No. 1.3e-06;
Matches 80; Conservative 4; Mismatches 115; Indels 90; Gaps 16

Qy	107	EKPSILVBKCISSPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNTYTLTYVHRSRL	166
Db	29	EKPKLV--KCRSPGK-----ETFCWPEPGADGGLPTNYTLTYHKEGE	69
Qy	167	EKIHCENIFREGYFGCSFDLTKVKDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVK	226
Db	70	TLIHCPD-YKTGGNSCVF--SKGHTSIWKWVITVAINQMGISSSDPLVHVHTYIVE	126
Qy	227	FDPPIHKLNSF---HNDD---LYVOMENPQN-----FISRCULFYEVEVNSQT---	E 269
Db	127	PEPP--ANLTLELKHPEDRKPYLWKNSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE	181
Qy	270	THNVFYVQAEKCNPEFERNVENTSCFMPVGYLPDTLNTVIRVKTNKLCTCYEDDKLWSNW	329

182	Db	THFTLQATQLKIFN-----LYPQKYLQVIR-----	CKPDHCYWSWSE	218
330	Qy	SOEWSIGCKKRNSTYYITWLLIVPVIIVAGAIIVLLYLKRLK-----	IIIPPIPPGGKIF	384
219	Db	SPSESSIQINDFPVKDTSMTWIFVAILLSAVICLIIMWVALKGYSMWTCILPPVPGP-KI-	PPVPGP-KI-	276
385	Qy	KEMFGDQNDDTLHWKKYDIY--EKOTKEE	411	
277	Db	-----KGFDPVHLLKGGKSEE	291	

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Job time : 27.2554 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 148.19 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARICGLWALLCAGG.....QTKETDSVVLLENKKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	1 IL3R1_HUMAN	P78552 homo sapien
2	2309.5	99.5	427	2 Q5USL4_HUMAN	Q5jgl4 homo sapien
3	2296.5	99.0	427	2 Q96BB4_HUMAN	Q96bb4 homo sapien
4	2291.5	98.8	426	2 Q59EG2_HUMAN	Q59eg2 homo sapien
5	2140	92.2	409	2 Q7YRV5_MACFA	Q7yrv5 macaca fasc
6	1939.5	83.6	423	2 Q863Z6_PIG	Q863z6 sus scrofa
7	1827	83.1	401	2 Q6U6T1_SHEEP	Q6u6t1 ovis aries
8	1878	80.9	405	2 Q95LPI_CANFA	Q95lfl canis famil
9	1696	73.1	424	1 IL3R1_MOUSE	Q90030 mus musculu
10	1690	72.8	424	2 Q8C1Z3_MOUSE	Q8clz3 mus musculu
11	1687	72.7	426	2 Q561K3_RAT	Q561k3 rattus norv
12	1680	72.4	424	2 Q8BNM4_MOUSE	Q8bnm4 mus musculu
13	1654	71.3	426	2 Q8VHC2_RAT	Q8vhc2 rattus norv
14	1610	69.4	349	2 Q97597_BOVIN	Q97597 bos tauris
15	1524.5	65.7	279	2 Q9UDY5_HUMAN	Q9udy5 homo sapien
16	977.5	42.1	252	2 Q8VDP7_MOUSE	Q8vdp7 mus musculu
17	463	20.0	226	2 Q6ZW70_HUMAN	Q6zw70 homo sapien
18	329	14.2	386	1 IL3R2_CANFA	Q951f0 canis famil
19	318	13.7	415	1 IL3R2_MOUSE	P21183 mus musculu
20	296.5	12.8	420	1 IL3R4_HUMAN	Q01344 homo sapien
21	294.5	12.7	380	1 IL3R2_HUMAN	Q14627 homo sapien
22	294.5	12.7	420	2 Q14633_HUMAN	Q14633 homo sapien
23	287.5	12.4	383	2 Q88786_MOUSE	Q88786 mus musculu
24	282.5	12.2	396	2 Q14631_HUMAN	Q14631 homo sapien
25	279.5	12.0	415	2 Q920K4_CAVPO	Q920k4 cavia porce
26	277	11.9	385	2 Q8VHK6_RAT	Q8vnh6 rattus norv
27	273.5	11.8	414	2 Q920B8_RAT	Q920b8 rattus norv
28	272.5	11.7	414	2 Q99FS3_RAT	Q99fs3 rattus norv
29	269.5	11.6	348	2 Q8AUP2_CHICK	Q8aup2 gallus gall
30	263	11.3	391	2 Q6UJN8_TETNG	Q6uan8 tetraodon n
31	262.5	11.3	374	2 Q8AV07_CHICK	Q8av07 gallus gall

32	242.5	10.5	393	2 Q5US16_XENLA	Q5u516 xenopus lae
33	241.5	10.4	404	2 Q90XP8_ONCMY	Q90xp8 oncothynchu
34	229	9.9	333	2 Q15469_HUMAN	Q15469 homo sapien
35	228	9.8	400	1 CSF3R_HUMAN	P15509 homo sapien
36	228	9.8	400	2 Q4V311_HUMAN	Q4v311 homo sapien
37	225	9.7	335	2 Q8NHV7_HUMAN	Q8nhv7 homo sapien
38	221.5	9.5	410	2 Q4V312_HUMAN	Q4v312 homo sapien
39	216.5	9.3	415	2 Q66IN1_XENLA	Q66in1 xenopus lae
40	215	9.3	368	2 Q76KD0_PIG	Q76kd0 sus scrofa
41	215	9.3	368	2 Q8S071_PIG	Q8sq71 sus scrofa
42	211	9.1	368	2 Q68FU6_RAT	Q68fu6 rattus norv
43	207	8.9	373	1 IL2RG_CANFA	P43021 canis famil
44	205.5	8.9	369	1 IL2RG_MOUSE	P43002 mus musculu
45	203.5	8.8	278	2 Q8VHR8_RAT	Q8vhr8 rattus norv

ALIGNMENTS

RESULT 1

IL3R1_HUMAN STANDARD; PRT; 427 AA.
ID IL3R1_HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q95646; Q99656;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213al antigen).
DE 13RA-1) (CD213al antigen).
GN Name=IL13RA1; Synonyms=IL13R, IL13RA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;
RA Miloux B.; Laurent P.; Bonnin O.; Lupker J.; Caput D.; Vita N.;
RA Ferrara P.;
RT "Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B-cell;
RX Gauchat J.F.M.; Schlagenhaut B.; Feng N.P.; Moser R.; Yanage M.; Jeannin P.; Alouani S.; Elson G.; Notarangelo L.D.; Wells T.; Eugster H.P.; Bonnefoy J.Y.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;
RA Aman M.J.; Tayebi N.; Obiri N.I.; Puri R.K.; Modi W.S.; Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX Wada M.; Hisano T.; Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Pancreas;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udgin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Kozlowski J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity.
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
CC and possibly other components.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
CC skeletal muscle and ovary; lowest levels in brain, lung and
CC kidney. Also found in B-cells, T-cells and endothelial cells.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y10659; CAAT1669.1; -; mRNA.
DR EMBL; Y09328; CAAT0508.1; -; mRNA.
DR EMBL; U62858; AAB37127.1; -; mRNA.
DR EMBL; U81379; AAD00510.3; -; mRNA.
DR EMBL; BC009960; AAK09960.1; -; mRNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR HGNC; HGNC:5974; IL13RA1.
DR H-InvDB; HIX0017008; -.
DR MIM; 300119; -.
DR GO; GO:0005898; C:plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO REC S_F2; 1.
KW Glycoprotein; Receptor; Signal; Transmembrane.
FT SIGNAL 1 21 Potential
FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.
FT TOPO_DOM 22 343 Extracellular (Potential).
FT TRANSMEM 344 367 Potential.
FT TOPO_DOM 368 427 Cytoplasmic (Potential).
FT MOTIF 327 331 WSXWS motif.
FT MOTIF 374 382 Box 1 motif.
FT CARBOHYD 37 37 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 61 61 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 235 235 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 265 265 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 293 293 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 329 329 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 46 95 Potential.
FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.
FT CONFLICT 130 130 T -> I (in Ref. 3).
FT CONFLICT 358 358 G -> D (in Ref. 3).
SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
Query Match 99.5%; Score 2309.5; DB 1; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.1e-167;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPALCGLWALLLLCAGGGGGG--APTETQPPVTLNLSVSVENLCTVITWNPPEGASS 59
DB 1 MEWPALCGLWALLLLCAGGGGGGAAPTETQPPVTLNLSVSVENLCTVITWNPPEGASS 60
QY 60 NCSLWTFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGQCSSTNESEKPSILVEKICIS 119
DB 61 NCSLWTFSHFGDKQDKKIAPETRRSIEVPLNERICLVGSGQCSSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELQCIWHNLNLSYKMSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREG 179
DB 121 PEGDPESAVTELQCIWHNLNLSYKMSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREG 180
QY 180 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIKNTSFHN 239
DB 181 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIKNTSFHN 240
QY 240 DDLYVQWENPQNFISRCFLFYEVVNSOTETHNVFVQEAECENPERFERNVENTSCFMPV 299
DB 241 DDLYVQWENPQNFISRCFLFYEVVNSOTETHNVFVQEAECENPERFERNVENTSCFMPV 300
QY 300 GVLPTDLTVTRVTKNKLCYEDDKLWSNWSQMSIGKRNSTLYITMLLIVPVI VAGAI 359
DB 301 GVLPTDLTVTRVTKNKLCYEDDKLWSNWSQMSIGKRNSTLYITMLLIVPVI VAGAI 360
QY 360 IVLLLYLKLKLIIPPIPDGKIPKEMFGDQNDTLHWKQDIYKQTKETDSVVLIE 419
DB 361 IVLLLYLKLKLIIPPIPDGKIPKEMFGDQNDTLHWKQDIYKQTKETDSVVLIE 420
QY 420 NLKKSQ 426
DB 421 NLKKSQ 427
RESULT 2
Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5JSL4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Interleukin 13 receptor, alpha 1.
GN Names=IL13RA1; ORFNames=RP13-12804.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AL391280; CAI41410.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:Hematopoietin/interferon-class (D200-domain. . . ; IEA.
DR InterPro; IPR004872; Fireceptor activity; IEA.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.

```
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;

Query Match 99.5%; Score 2309.5; DB 2; Length 427;
Best Local Similarity 99.8%; Pred. No. 6.1e-167;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MEWPARLCGLWALLLCAGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60

Qy 60 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNSEKPSILVEKCIISP 119
Db 61 NCSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCTNSEKPSILVEKCIISP 120

Qy 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHOCENIFREG 180

Qy 180 QYFGCSPLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 239
Db 181 QYFGCSPLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKDPDPHIKNLSFHN 240

Qy 240 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCILFYEVVNNSTQTHNVFYQEAECENPEFERNVENTSCFMVP 300

Qy 300 GVLPTDLNTVIRVKTNKLCEYEDDKLWSNQSEMSIGKKNRSTLYITMLLIYPVIVAGAI 359
Db 301 GVLPTDLNTVIRVKTNKLCEYEDDKLWSNQSEMSIGKKNRSTLYITMLLIYPVIVAGAI 360

Qy 360 IVLLYLKRLKLIIPPPIDPKIKPMFGQNDTTLHWKDYDIYEKOTKESTDSVLLIE 419
Db 361 IVLLYLKRLKLIIPPPIDPKIKPMFGQNDTTLHWKDYDIYEKOTKESTDSVLLIE 420

Qy 420 NLKQASQ 426
Db 421 NLKQASQ 427

RESULT 3
Q56BB4 HUMAN ;
ID Q56BB4 HUMAN PRELIMINARY; PRT; 427 AA.
AC Q56BB4; Q5WY08;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209849; BAD93086.1; -; mRNA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 426 AA; 4855 MW; 342A3A6F7347261B CRC64;

Query Match 98.8%; Score 2291.5; DB 2; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.4e-165;
Matches 424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 EWPALCGLWALLLCAGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPPGASSN 60
Db 1 EWPALCGLWALLLCAGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPPGASSN 60
QY 61 CSLWYFSHFQDKQKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 120
Db 61 CSLWYFSHFQDKQKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 120
QY 121 EGPESAVTELCITWNLSTYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 180
Db 121 EGPESAVTELCITWNLSTYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREG 180
QY 181 YFGCSFDLTQKVDSSFEQSHVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSF 240
Db 181 YFGCSFDLTQKVDSSFEQSHVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSF 240
QY 241 DLVVOENPQNFISRCIFYEVEVNNSTETHNFYVQEAKECENPEFERNVENTSCF 300
Db 241 DLVVOENPQNFISRCIFYEVEVNNSTETHNFYVQEAKECENPEFERNVENTSCF 300
QY 301 VLPDTLNTVIRVKTNKLCEYDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAI 360
Db 301 VLPDTLNTVIRVKTNKLCEYDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAI 360
QY 361 VLLLYLKLKIIIFPPIDPGKIFKEMFGQNDTLHWKYDIYEKOTKEETSDSVLIEN 420
Db 361 VLLLYLKLKIIIFPPIDPGKIFKEMFGQNDTLHWKYDIYEKOTKEETSDSVLIEN 420
QY 421 LKKSQ 426
Db 421 LKKSQ 426

RESULT 5
QYRV5_MACFA PRELIMINARY; PRT; 409 AA.
AC QYRV5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13RA1;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Maccarone P., Drinkwater C.C., Nash A.D.;
RA "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY312267; AAF78901.1; -; mRNA.

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DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR002996; Cytok_recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON_TER 1
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 92.2%; Score 2140; DB 2; Length 409;
Best Local Similarity 96.8%; Pred. No. 4.3e-154;
Matches 394; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 19 GGGGGGGAAPTETQPPVTNLVSVENLCTVIWTPNPPGASSNCLWYFSHFQDKQKIA 78
Db 2 GGGGGGGAAPTETQPPVTNLVSVENLCTVIWTPNPPGASSNCLWYFSHFQDKQKIA 61
QY 79 PETRSIEVPLNERICLVGSCSTNESEKPSILVEKCISSPPGDPESAATELCIWHNL 138
Db 62 PETRSIEVPLNEKICLVGSCSTNESEKPSILVEKCISSPPGDPESAATELCIWHNL 121
QY 139 SYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGYFGCSFDLTQKVDSSFEQ 198
Db 122 SYMQCSWLPGRNTSPDTNTLYYHRSLEKIROCEIYKEGYFGCSFDLTQKVDSSFEQ 181
QY 199 HSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPHINKLSFHNDLHYVQENPQNFISRC 258
Db 182 HSVQIMVKDYAGIKPSFNIVPLTSRVKDPDPHINKLSFHNDLHYVQENPQNFISRC 241
QY 259 YEVEVNNSTETHNFYVQEAKECENPEFERNVENTSCFVPGVLPDTLNTVIRVKTNKL 318
Db 242 YEVEVNNSTETHNFVQEAKECENPEFERNVENTSCFVPGVLPDTLNTVIRVKTNKL 301
QY 319 CYEDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 378
Db 302 CYEDDKLSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 361
QY 379 DPGKIFKEMFGQNDTLHWKYDIYEKOTKEETSDSVLIENLKASQ 426
Db 362 DPGKIFKEMFGQNDTLHWKYDIYEKOTKEETSDSVLIENLKASQ 409

RESULT 6
Q863Z6_PIG PRELIMINARY; PRT; 423 AA.
AC Q863Z6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarlenga D.S., Dawson H., Krangel H., Solano-Aguilar G.,
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
RT 1-chains; effects of experimental Toxoplasma gondii, Ascaris suum and
RT Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234 (2004).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or

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CC activation (By similarity).
DR EMBL; AY266142; AAP23301.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn recept B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
DR KW Receptor; Transmembrane.
DR SQ SEQUENCE 423 AA; 47984 MW; EA636FE6BCA533D9 CRC64;

Query Match 83.6%; Score 1939.5; DB 2; Length 423;
Best Local Similarity 84.3%; Pred. No. 7.7e-139;
Matches 359; Conservative 25; Mismatches 39; Indels 3; Gaps 2;

QY 1 MWPRLCGLWALLLCAGGGGGGAPPTETPPVTNLSVSVENLCTVITWNPPEGASN 60
DB 1 MERPARLYGLWALLFCA--GGGGLAAPAETQPPVTNLSVSVENLCTVITWNPPEGASN 58
QY 61 CSLWYFHFHGKQDKKIAPETRRSIEVPLNERICLVQVSGQSTNESEKPSILVEKCI 120
DB 59 CSLWYLSHFGNKQDKKIPTETRRSEVEFLNERICLVQVSGQSTNESEKPSILVEKCI 118
QY 121 EGDPSAVTELCIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHOCENIFREGQ 180
DB 119 EGDPSAVTELCVQVWHNRYMKCTWLPGRNTSPDNTYLYYWHRSLEKIHOCENIREDQ 178
QY 181 YFGCSFDLTWKVDSFEQSHVQIMVKNAGIKPSFNIVPLTSRVKPPPHIKNLSFHD 240
DB 179 HIACSFALTWKVDSNFDS-SVQIMVKNAGIKRPAFISVPSSSHVVKPPPHIKLSFQNG 237
QY 241 DLYVQWNPQNFISCLFYEVEVNSQETNNVYVQAEKCNPEFERNVENTSCFMVPG 300
DB 238 DLYVQWNPQNFYSRCLSYQVEVNTQAKTHDIFYVEBAKQNSFEGLGCMICFMVPG 297
QY 301 VLPDPLNTVIRVKTNKLCEYDDKLSWNSQMSIGKRNSTLYITMLIVPVIVAGAIL 360
DB 298 VLPDPLNTVIRVKTNKLCEYDDKLSWNSQMSIGQKANPTFYITLLIIPVIVAAAIL 357
QY 361 VLLYLKELKLIIFPPIDPGKIFKFMFGDQNDTLHWKCYDIYEKQTKBEETSDSVLJEN 420
DB 358 VLLYLKELKLIIFPPIDPGKIFKFMFGDQNDTLHWKCYDIYEKQTKBEETSDSVLJES 417
QY 421 LKQASQ 426
DB 418 LKQASQ 423

RESULT 7
Q6U6T1 SHEEP PRELIMINARY; PRT; 401 AA.
AC Q6U6T1.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Interleukin 13 receptor alpha 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RT "Cloning of the sheep interleukin 13 receptor alpha 1 cDNA.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY377582; AAQ83584.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR002996; Cytokn recept B/G.
DR KW Receptor; Transmembrane.
DR SQ SEQUENCE 423 AA; 47984 MW; EA636FE6BCA533D9 CRC64;

Query Match 83.1%; Score 1927; DB 2; Length 401;
Best Local Similarity 87.8%; Pred. No. 6.4e-138;
Matches 352; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 26 APETQPPVTNLSVSVENLCTVITWNPPEGASNCISLWYFHFHGKQDKKIAPETRRS 85
DB 1 APRESHPVPTNLSVSVENLCTIITWNPPEGASNCISLWYFHFHGKQDKKIAPETRRSK 60
QY 86 EVPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCSW 145
DB 61 EVPLNERICLVQVSGQSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCTW 120
QY 146 LPGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEQSHVQIMV 205
DB 121 LPGNTSPDNTYLYYWHRSLEKIHOCENIYREGQHIACSFNLTKVDSFEQSHVQIMV 180
QY 206 KDNAGIKPSFNIVPLTSRVKPPPHIKNLSFHDNLDLYVQWNPQNFISRCLFYEVEVNN 265
DB 181 KDNAGIKPSFNIVPLTSRVKPPPHIKNLSFQNGDLYVQWNPQNFOSKCLSYEVEVNN 240
QY 266 SQTETHNVYVQAEKCNPEFERNVENTSCFMVPGVLPDPLNTVIRVKTNKLCEYDDKL 325
DB 241 SHAETHDIFYVEBAKQNTFERNLEGTICFMVPGVLPDPLNTVIRVKTNKLCEYDDKL 300
QY 326 WSNWSQMSIGKRNSTLYITMLIVPVIVAGAILVLLYLKELKLIIFPPIDPGKIFK 385
DB 301 WSNWSQMSIGQKANPTFYITLLIIPVIVAAAILVLLYLKELKLIIFPPIDPGKIFK 360
QY 386 EMFGDQNDTLHWKCYDIYEKQTKBEETSDSVLJENLKQASQ 426
DB 361 EMFGDQNDTLHWKCYDIYEKQTKBEETSDSVLJENLKQAAQ 401

RESULT 8
Q95LF1 CANFA PRELIMINARY; PRT; 405 AA.
AC Q95LF1.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Interleukin 13 receptor alpha chain 1 (Fragment).
GN Name=IL13R1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";
RL Vet. Immunol. Immunopathol. 79:181-195 (2001).
DR EMBL; AF314532; AAL14886.1; -, mRNA.
DR Ensembl; ENSCAFG00000018359; Canis familiaris.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn recept B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003332; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
DR KW Receptor.
DR SQ SEQUENCE 401 AA; 47984 MW; EA636FE6BCA533D9 CRC64;
DB 361 EMFGDQNDTLHWKCYDIYEKQTKBEETSDSVLJENLKQAAQ 401
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SQ SEQUENCE 405 AA; 46328 MW; 926ELIAC7BE5E3F42 CRC64;
Query Match 80.9%; Score 1878; DB 2; Length 405;
Best Local Similarity 85.24; Pred. No. 3.4e-134;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 22 GGGAGTETOPPTNLSVSVENLCTVITWNPPEGASSNCISLWVFGHFGDKDKKIAPET 81
DB 1 GGVAAPTETOPPTNLSVSVENLCTVITWNPPEGASSNCISLWVFGHFGDKDKKIAPET 60

QY 82 RRSIEVPLNERICLQVGSQCTNESEKPSILVKICISPPEDGPESAVTELQCIWHNLSYM 141
DB 61 HRSKEVPLNERICLQVGSQCTNESEKPSILVKICISPPEDGPESAVTELQCIWHNLSYM 120

QY 142 KCSWLPGRNTSPDNTYLYIYHRSLEKIHCENIFREGQVFGSPDLTKVKDSSPQHSV 201
DB 121 KCTWLPGRNTSPDNTYLYIYHRSLEKIHCENIFREGQVFGSPDLTKVKDSSPQHSV 180

QY 202 QIMVKDNAGIKPSINIVLTSRKVDPDPHINKLSFHNDDLYVOMENPONFISRCIFYEV 261
DB 181 QIMVKDNARKIRSFNIVLTSRKVDPDPHINKLSFHNDDLYVOMENPONFISRCIFYEV 240

QY 262 EVNNSQTEHNVFYOEAKENFEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYE 321
DB 241 EVNNSQTEINDIFYVEAKQNSEFEGNLBGTICFMVPGVLPDTLNTVIRVTKNLCYE 300

QY 322 DDKLWNSWSEMGIGKRRNSTLYITMLLIVPVTVAGAIIVLLYLKRLKIIIPPTIPDPG 381
DB 301 DDKLWNSWQAMSGENTDPTFTYITMLLATQVIVAGAIIVLLYLKRLKIIIPPTIPDPG 360

QY 382 KIFKEMFGQDNDTLHWKYDIYEKOTKETSDSVLIENLKASQ 426
DB 361 KIFKEMFGQDNDTLHWKYDIYEKOTKETSDSVLIENLKASQ 405

RESULT 9
IL13R1_MOUSE
ID IL13R1_MOUSE STANDARD; PRT; 424 AA.
AC G09030; Q7T727;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain, precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
GN Names=IL13ra1; Synonyms=IL13r, IL13ra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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QY 121 EGDPSAVTEQCIWHNLSYKCSWLPGRNTSPDNTYTLTYWHSLEKIHOCENIFREGQ 180
 DB 120 EGDPSAVTEQCIWHNLSYKCSWLPGRNTSPDNTYTLTYWHSLEKSRQENIYREGQ 179
 QY 181 YFGSFDLTIVKQDSFEQSHQVQIMVKONAGIKFSPNIVPLTSRVKPPPHIKNLSFEND 240
 DB 180 HIACSFKLTKV-EPSFEHQNVQIMVKONAGIKRPSCKIVSLTSVVKPDPHKKLLKNG 238
 QY 241 DLYVQWENPQIFISCLPYEVEVNNSTQETNRVFFVQEAKEPNFERNVENTSCFVVP 300
 DB 239 ALLVQWKNPQFNRSLCTYEVEVNNSTQETNRVFFVQEAKEPNFERNVENTSCFVVP 298
 QY 301 VLPDTLNTVRVTKNLCYEDDKLWNSQEMSGKGRNSTLYITMLLIVPVLVAGAIL 360
 DB 299 VLADAVYTVRVKTKNLCYEDDKLWNSQEMSGKGRNSTLYITMLLIVPVLVAVAVI 358
 QY 361 VLLYLKRLKLIIFPPIPKFKEMFGDQNDTDLHWKCYDIYEKQKEETSDSVLIEN 420
 DB 359 ILLFVLRKLIIFPPIPKFKEMFGDQNDTDLHWKCYDIYEKQKEETSDSVLIEN 418
 QY 421 LKKA 425
 DB 419 LKKA 423

RESULT 10
 ID Q8C123 MOUSE PRELIMINARY; PRT; 424 AA.
 AC Q8C123
 DT 01-MAR-2003 (TreeBrel. 23, Created)
 DT 01-MAR-2003 (TreeBrel. 23, Last sequence update)
 DE Mus musculus embryo RCB-0549 C1e-H3 cDNA, RIKEN full-length enriched
 DE library, clone:G430044I06 product:interleukin 13 receptor, alpha 1,
 DE full insert sequence.
 GN Name=Il13ral;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Embryo;
 RC The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipipette sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC EMBL; AK099984; BAC1028.1; -; mRNA.
 DR MGI; MGI:105052; Il13ral.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003532; Hemtpnrecept_F2.
 DR SMART; SM0060; FN3; 1.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor.
 SQ SEQUENCE 424 AA; 48371 MW; 4B45EB0876EB83F CRC64;
 Query Match 72.8%; Score 150; DB 2; Length 424;
 Best Local Similarity 74.6%; Pred. No. 7e-120;
 Matches 317; Conservative 40; Mismatches 66; Indels 2; Gaps 2;
 QY 1 MEMPARLGLWALLCAGGGGGGAPETQPPVNTLSVSVENLCTVIWTNPPGASGN 60
 DB 1 MARPALLGELLVLLWTATVGVAAA-TEVQPPVNTLSVSVENLCTVIWTNPPGASPN 59
 QY 61 CSLWTFSPGDKQDKKIADPTRRSIEVPLNERICLVQVSGCSTNESEKPSILVEKICSP 120

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Db 10-036-568a-4.rup
Qy 121 EGDPSAVTELCIWHNLSYMKCSWLPGRNTPPTNTLYYHRSLEKIHQCNIFREGQ 180
Db 120 EGDPSAVTELCIWHNLSYMKCSWLPGRNTPPTNTLYYHRSLEKIHQCNIFREGQ 179
Qy 181 YFGCSFDTLVKSDSSFEQHSVOIMVKNAGKIPESFNIVPLTSRVKDPDPHKNLSFND 240
Db 180 HIACSFKLTKV-EPSEFHQNVQIMVKNAGKIPESFNIVPLTSRVKDPDPHKNLSFND 238
Qy 241 DLVYQWENPQNFISRCIFYEVEVNNSTQTHNVPYQAEKCNPEPNNVENTSCFVVP 300
Db 239 ALLVQWKNPQNFISRCIFYEVEVNNSTQTHNVPYQAEKCNPEPNNVENTSCFVVP 298
Qy 301 VLPDNLTVNRIRVTKNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIIPVIVAGII 360
Db 299 VLADAVTVRVTKNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIIPVIVAVI 358
Qy 361 VLLIYKRLKIIIPPPDPGKIPKEMFGQNDTLHWKYDIYEKQKEETSDSVLIEN 420
Db 359 ILLFYKRLKIIIPPPDPGKIPKEMFGQNDTLHWKYDIYEKQKEETSDSVLIEN 418
Qy 421 LKXAS 425
Db 419 LKXAA 423

RESULT 11
Q561K3 RAT PRELIMINARY; PRT; 426 AA.
ID Q561K3 RAT PRELIMINARY; PRT; 426 AA.
AC Q561K3 2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1.
GN Name=il13ral;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -i- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
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CC surface receptor binding (By similarity).
CC -i- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
CC -i- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; BC093615; AAH93615.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 426 AA; 48464 MW; 7D2E05B7A6520A8C CRC64;

Query Match 72.7%; Score 1687; DB 2; Length 426;
Best Local Similarity 74.5%; Pred. No. 1.2e-119;
Matches 318; Conservative 43; Mismatches 62; Indels 4; Gaps 3;

Qy 1 MEWPARLCGLWALLCAGGGGGGGGAPTETPPVTHLSVSVENLCTVIWTWNPPEGASN 60
Db 1 MARPAWLGELLVLLFAASLDQVALA-TEVQPPVTNLSVSVENLCTVIWTWNPPEGASN 59
Qy 61 CSLWYFSGDKDKKIAPEATRESIEVPLNERICLOVGSOCSTNSESKEPSILVEKICSP 120
Db 60 CSURYFSGHDDQDDKIAPEATRRKKELPLNEKICLOVGSOCSTNSESKEPSILVEKICSP 119
Qy 121 EGDPSAVTELCIWHNLSYMKCSWLPGRNTPPTNTLYYHRSLEKIHQCNIFREGQ 180
Db 120 EGDPSAVTELCIWHNLSYMKCSWLPGRNTPPTNTLYYHRSLEKIHQCNIFREGQ 179
Qy 181 YFGCSFDTLVKSDSSFEQHSVOIMVKNAGKIPESFNIVPLTSRVKDPDPHKNLSFND 240
Db 180 HIGCSFKLTKV-ESNYEHHNIQIMVKNAGKIPESFNIVPLTSRVKDPDPHKNLSFND 238
Qy 241 DLVYQWENPQNFISRCIFYEVEVNNSTQTHNVPYQAEKCNPEPNNVENTSCFVVP 298
Db 239 ALFVQWKNPQNFISRCIFYEVEVNNSTQTHNVPYQAEKCNPEPNNVENTSCFVVP 298
Qy 299 PGVLPDNLTVNRIRVTKNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIIPVIVAG 358
Db 299 PGVLPDNLTVNRIRVTKNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIIPVIVAG 358
Qy 359 IIVLLYKRLKIIIPPPDPGKIPKEMFGQNDTLHWKYDIYEKQKEETSDSVLI 418
Db 359 IIVLLYKRLKIIIPPPDPGKIPKEMFGQNDTLHWKYDIYEKQKEETSDSVLI 418
Qy 419 ENLKAS 425
Db 419 ENLKAA 425

RESULT 12
Q8BNM4 MOUSE PRELIMINARY; PRT; 424 AA.
ID Q8BNM4 MOUSE PRELIMINARY; PRT; 424 AA.
AC Q8BNM4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone: C430004G12 product: interleukin 13 receptor, alpha 1,
DE full insert sequence.
DE Name=il13ral;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
```

"High-efficiency full-length cDNA cloning.";
[2]
Meth. Enzymol. 303:19-44(1999).
[2]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Whole body;
DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Whole body;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
-I- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
EMBL; AK082889; BAC38670.1; -; mRNA.
MG1; MG1105052; Ill3ral.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
InterPro; IPR003532; Hemtpnrecept_F2.
SMART; SMO0060; FN3; 1.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
Receptor.
SEQUENCE 424 AA; 48341 MW; E07ECBD276D67BBS CRC64;
Query Match 72.4%; Score 1680; DB 2; Length 424;
Best Local Similarity 74.1%; Pred. No. 4e-119;
Matches 315; Conservative 42; Mismatches 66; Indels 2; Gaps 2;
QY 1 MEWPARLCGLWALLCAGGGGGGGGAPETPTPTPTNLVSVSVENLCTVITWNPPEGASGN 60
DB 1 MARPALLGELLVLLLTATVCGVAAA-TEVQPPVPTNLVSVSVENLCTIITWTPPEGASPN 59
61 CSLWYFSGHFGDKQDKKIAPETRRSIEVPLNERICLVGSGQCSSTNESEKPSILVEKCI 120
DB 60 CTLYFYSFHDQDKKIAPETRRKEELPLDEKICLVGSGQCSANESKPSPLVKKCISPP 119
121 EGDPEAVTELCIWHNLNLYNKCWLPGNRTSPDNTYLYWHRSLKIKHOCENIFREGQ 180
DB 120 EGDPEAVTELCIWHNLNLYNKCWLPGNRTSPDNTYLYWHRSLKIKHOCENIFREGQ 179
181 YFGSCFDLTKVQDSFEQHSVQIMVKONAGKIKSFNVLPTSRVKPDPHPHKLNLSEND 240
DB 180 HIACSEKLTQV-EPSFEHQVQIMVKONAGKIRPSCKIVLSVTVKPPPHKHLQLQNG 238
241 DLVYQWENPQFISRCLEFYEVEVNNSTQETHNVYVQBAKCNPFERNVENTSCFVPG 300
DB 239 ALLVQWQKQPNFRSCLTYEVEVNTQDRENLVEEDKQNSDRMEGTSCEFPLPG 298
301 VLPDLTNTVRIRVTKNKLCEYDDKLWSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIL 360
DB 299 VLADAVYTVRVQTNKLCFDDNQLNSDWSAQSIGKEPNSTFTYTMLLTIPFVAVAVI 358
361 VLLLYLKLKILIIIPPDPGKIPKEMFGDNDLTLHWKDYIYEKQKEETDSVVLLEN 420
DB 359 ILLFYLERLKIIFPPDPGKIPKEMFGDNDLTLHWKDYIYEKQKEETDSVVLLEN 418
421 LKKA 425
419 LKKA 423
RESULT 13
Q8VHC2 RAT PRELIMINARY; PRT; 426 AA.
ID Q8VHC2 RAT PRELIMINARY; PRT; 426 AA.
AC Q8VHC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-13 receptor alpha 1.
Name=Il13ral;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fisher F344;
RX MEDLINE=21458304; PubMed=11573960; DOI=10.1006/bbrc.2001.5682;
RA Pierrot C., Beniguel L., Begue A., Khalife J.;

"Expression of a functional IL-13Ralphal by rat B cells.",
 RT Blochem. Biophys. Res. Commun. 287:969-976 (2001).
 RL -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 DR EMBL; AY044251; AAK94870.1; -; mRNA.
 DR PIR; JC7773; JC7773.
 DR Ensembl; ENSRNOG0000013170; Rattus norvegicus.
 DR RGD; 628741; Il13ral.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytkn recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 DR Receptor; Transmembrane.
 KW SEQUENCE 426 AA; 48510 MW; 08BFB0E31D9D3C47 CRC64;
 SQ
 Query Match 71.3%; Score 1654; DB 2; Length 426;
 Best Local Similarity 73.3%; Pred. No. 3.8e-117;
 Matches 313; Conservative 43; Mismatches 67; Indels 4; Gaps 3;
 QY 1 MEWPARLCGLWALLLCAGGGGGGAGPTTOPVTNLSVSVENLCTVITWNPPEGASSN 60
 DB 1 MARPAWLGELLVLLFAASLDQVALA-TEVQPPVTNLSVSVENLCTVITWNPPEGASPN 59
 QY 61 CSLWYFSHFGDKDKKIAPETRISIEVPLNERICLQVGSQCSTNESEKPSILVEKICISPP 120
 DB 60 CSURYFSHFDDQDKKIAPETRKRKELPLNEKICLQVGSQCSTNESEKPSILVEKICISPP 119
 QY 121 EGDPEASVTELOCIWHNLSYMKSWLPGRNTSPDNTYTLTYWHRSLKIHOCENIFREGQ 180
 DB 120 RRGSEASVTELOCTWHNLSYMKSWLPGRNTSPDNTYTLTYWYSSLGKSLQCENIHREGQ 179
 QY 181 YFGCSFDLTKVDDSSFEQHSVQIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFIND 240
 DB 180 HIGCSFKLTKV-ESNYEHNNIQIMVKNAGKIRPSYKIVSFSTNYPKPPPHIKHLFLKNG 238
 QY 241 DLVQVENPQNFISRLCFYEVEVNNSTQETH--NVFYQAEAKCENPEFERNVENTSCFMV 298
 DB 239 ALFQWKNPQNFESRCLSYEVEVNNSTQETH--NVFYQAEAKCENPEFERNVENTSCFMV 298
 QY 299 PGVLPTDLTNTVRIRVTKNKLCEYDDKXLSNWSQEMSIGKRNSTLIYITMLLIVPVI VAGA 358
 DB 299 PGVLANTVTVVRVTKNKLCPDDNDLMSNWEALSIGKEPNSTFTYTTMLLIIPVFAVV 358
 QY 359 IIVLLYLKRLKLIIPPPIDPKGIPKEMFGQNDOTLHWKKYDIYEQTKTEEDTSVVLI 418
 DB 359 IITLLFYLKRLKLIIPPPIDPKGIPKEMFGQNDOTLHWKKYDIYEQTKTEEDTSVVLI 418
 QY 419 ENLKKS 425
 DB 419 ENLKKA 425
 RESULT 14
 O97597_BOVIN PRELIMINARY; PRT; 349 AA.
 AC O97597;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Interleukin-13 receptor alpha-1 chain (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiathalia; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 [1]
 NUCLEOTIDE SEQUENCE.
 MEDLINE=20080132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
 Trigna W.L.; Brown W.C.; Bates D.M.;
 RA "Functional implications for signaling via the IL4R/IL13R complex on
 RT bovine cells";
 RL Vet. Immunol. Immunopathol. 72:73-79 (1999).
 DR EMBL; AF074402; AAC98147.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytkn recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39644 MW; D61A4C91B81940A6 CRC64;
 Query Match 69.4%; Score 1610; DB 2; Length 349;
 Best Local Similarity 84.5%; Pred. No. 6.5e-114;
 Matches 295; Conservative 17; Mismatches 37; Indels 0; Gaps 0;
 QY 34 VTNLSVSVENLCTVITWNPPEGASSNCSLMYFSHFGDKDKKIAPETRISIEVPLNERI 93
 DB 1 VTNLSVSVENLCTVITWNPPEGASPNCSLMYFSHFGNKDKKIAPETRHSKEVPLNERI 60
 QY 94 CLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKSWLPGRNTSP 153
 DB 61 CLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKSWLPGRNASP 120
 QY 154 DTNTYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDDSSFEQHSVQIMVKNAGKIK 213
 DB 121 DPNYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDDSSFEQHSVQIMVKNAGKIS 180
 QY 214 PSFNIIVPLTSRVKPPPHIKNLSFINDLIYQWENPQNFISRLCFYEVEVNNSTQETHV 273
 DB 181 PSFNIIVPLTSRVKPPPHIKNLSFONGDLYVQWNTNPNQFQSQCLCYEVEVINSHAETHDI 240
 QY 274 FYVQAEAKCENPEFERNVENTSCFMVPGVLPTDLTNTVRIRVTKNKLCEYDDKXLSNWSQEM 333
 DB 241 FYVQAEAKCENPEFEGNLEGTCIFMVPGLPDTLNTVRIRVTKNKLCEYDDKXLSNWSQAM 300
 QY 334 SIGKRNSTLIYITMLLIVPVI VAGAIIVLLYLKRLKLIIPPPIDPKG 382
 DB 301 SIGQKANQFYITMLLIPVIVAAVIVLLYLKRLKLIIPPPIDPKG 349
 RESULT 15
 O9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
 AC O9UDY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
 DE 1).
 GN Name=IL13RA1; ORFNames=RP13-12804.2-002;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 NUCLEOTIDE SEQUENCE.
 Wada M., Hisano T., Kuwano M.;
 RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC


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CC -|- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (by similarity).
CC -|- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (by similarity).
DR EMBL; U81380; AAD00511.2; -; mRNA.
DR EMBL; AL391280; CAI41409.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept B/G.
DR InterPro; IPR003532; Hematofn_recept F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_P2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;

Query Match 65.7%; Score 1524.5; DB 2; Length 279;
Best Local Similarity 99.3%; Pred. No. 1.5e-107;
Matches 276; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MFWPARLCGLWALLLCAGGGGGGGGAPTETQPPVTNLSVSVENLCTVITWNPPEGASS 60

Qy 60 NCSLWYFSGHFGDKQDKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 119
Db 61 NCSLWYFSGHFGDKQDKIAPETRRSIEVPLNERICLVGSCSTNESEKPSILVEKCI 120

Qy 120 PEGDPESAVTEIQCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTEIQCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHQENIFREG 180

Qy 180 QYFGCSFDLTVKYDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTVKYDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

Qy 240 DDLVYQWENPQNFIISRCLEFYEVEVNNSTQETHNVFYVQ 277
Db 241 DDLVYQWENPQNFIISRCLEFYEVEVNNSTQETHNVFYVR 278
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Job time : 152.19 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 115,507 Seconds
(without alignments)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEWPARLCGLWALLCAGGG.....QTKRETDVSVLIENLKASQ 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	4	US-10-671-697-9
2	2309.5	99.5	427	6	US-11-067-251-3
3	2302.5	99.2	427	5	US-10-850-270-4
4	2302	99.2	426	4	US-10-036-568-4
5	1878	80.9	405	3	US-09-828-995B-50
6	1878	80.9	405	4	US-10-753-159-50
7	1875.5	80.8	780	3	US-09-935-868-34
8	1875.5	80.8	793	3	US-09-313-942-32
9	1875.5	80.8	793	3	US-09-935-868-32
10	1875.5	80.8	793	4	US-10-287-035-32
11	1875.5	80.8	793	4	US-10-282-162-32
12	1875.5	80.8	793	6	US-11-134-114-32
13	1866.5	80.5	780	3	US-09-935-868-42
14	1866.5	80.5	782	3	US-09-935-868-48
15	1865.5	80.4	782	3	US-09-935-868-38
16	1865.5	80.4	782	3	US-09-935-868-52
17	1862	80.3	780	4	US-10-287-035-34
18	1853	79.9	780	4	US-10-287-035-42
19	1853	79.9	782	4	US-10-287-035-48
20	1853	79.8	782	4	US-10-287-035-54
21	1852	79.8	780	4	US-10-287-035-38
22	1852	79.8	782	4	US-10-287-035-52
23	1852	79.8	782	4	US-10-287-035-58
24	1784.5	76.9	664	5	US-10-850-270-10
25	1779.5	76.7	784	3	US-09-313-942-30
26	1779.5	76.7	784	3	US-09-935-868-30
27	1779.5	76.7	784	4	US-10-287-035-30

28	1779.5	76.7	784	4	US-10-282-162-30	Sequence 30, Appl
29	1779.5	76.7	784	6	US-11-134-114-30	Sequence 30, Appl
30	1769	76.2	322	3	US-09-825-561A-82	Sequence 82, Appl
31	1769	76.2	322	5	US-10-872-087-82	Sequence 82, Appl
32	1750	75.4	776	3	US-09-935-868-36	Sequence 36, Appl
33	1741	75.0	776	3	US-09-935-868-44	Sequence 44, Appl
34	1741	75.0	776	4	US-10-287-035-40	Sequence 40, Appl
35	1741	75.0	776	6	US-11-067-251-10	Sequence 8, Appl
36	1741	75.0	776	6	US-11-067-251-12	Sequence 10, Appl
37	1741	75.0	776	6	US-11-067-251-14	Sequence 12, Appl
38	1741	75.0	776	6	US-11-067-251-16	Sequence 14, Appl
39	1740	75.0	776	3	US-09-935-868-46	Sequence 16, Appl
40	1736	74.8	778	3	US-10-287-035-46	Sequence 46, Appl
41	1736	74.8	778	4	US-10-287-035-60	Sequence 46, Appl
42	1736	74.8	778	4	US-10-287-035-60	Sequence 60, Appl
43	1735	74.8	778	3	US-09-935-868-50	Sequence 50, Appl
44	1735	74.8	778	4	US-10-287-035-50	Sequence 50, Appl
45	1735	74.8	778	4	US-10-287-035-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9

Query Match 99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.6e-186;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEWPARLCGLWALLCAGGGGGG-APTEPPVTNLVSVENICTVTWNPPEGASS 59
DB 1 MEWPARLCGLWALLCAGGGGGGAAPTETPPVTNLVSVENICTVTWNPPEGASS 60
QY 60 NCSLWYFSGHFGDKDKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKICISP 119

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Db 61 NCSLWFSHFQDKQDKKIAPEPTRRSIEVPLNERICLVQVGSQCSNTESEKPSILVEKICSP 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 2
US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067, 251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
; US-11-067-251-3

Query Match : 99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.6e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWFSHFQDKQDKKIAPEPTRRSIEVPLNERICLVQVGSQCSNTESEKPSILVEKICSP 119
Db 61 NCSLWFSHFQDKQDKKIAPEPTRRSIEVPLNERICLVQVGSQCSNTESEKPSILVEKICSP 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427
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Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLKRLLKIIIFPPIDPPGKIFKEMFGDQNDLTLHWKKYDIYEKQTKETDSVVLLIE 419
Db 361 IVLLLYLKRLLKIIIFPPIDPPGKIFKEMFGDQNDLTLHWKKYDIYEKQTKETDSVVLLIE 420
Qy 420 NLKKSQ 426
Db 421 NLKKSQ 427

RESULT 3
US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU FSI301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 20039000437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
; US-10-850-270-4

Query Match : 99.2%; Score 2302.5; DB 5; Length 427;
Best Local Similarity 99.5%; Pred. No. 1e-187;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
Qy 60 NCSLWFSHFQDKQDKKIAPEPTRRSIEVPLNERICLVQVGSQCSNTESEKPSILVEKICSP 119
Db 61 NCSLWFSHFQDKQDKKIAPEPTRRSIEVPLNERICLVQVGSQCSNTESEKPSILVEKICSP 120
Qy 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVDSSEFEQHSVQIMVKDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHN 240
Qy 240 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCLFYEVEVNNSTQETHNVFVYQEAACENPFRNVENTSCFMVP 300
Qy 300 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 359
Db 301 GVLPDPTLNTVIRVKTNKLKYEDDDKLSWNSQEMSIGKKNSTLYITMLLIIVPVIAGAI 360
Qy 360 IVLLLYLKRLLKIIIFPPIDPPGKIFKEMFGDQNDLTLHWKKYDIYEKQTKETDSVVLLIE 419
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Db 361 IVLLLYLKLKLIIFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 420
Qy 420 NLKASQ 426
| | | | |
Db 421 NLKASQ 427

RESULT 4
US-10-036-568-4
; Sequence 4, Application US/10036568
; Publication No. US20020090682A1
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian G.
; TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: Davies cc
; CURRENT APPLICATION NUMBER: US/10/036,568
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US/09/051,843
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4

Query Match 99.2%; Score 2302; DB 4; Length 426;
Best Local Similarity 99.3%; Pred. No. 1.1e-187;
Matches 423; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NEWPARLGLWALLLCAGGGGGGAGTETQPPVTNLVSVENLCTVIWNPPEGASSN 60
| | | | |
Db 1 NEWPARLGLWALLLCAGGGGGGAGTETQPPVTNLVSVENLCTVIWNPPEGASSN 60

Qy 61 CSLWYFHFHFGDKDKKIAPIETRRSIEVPLNERICLVGSGQSTNESEKPSILVEKICISPP 120
| | | | |
Db 61 CSLWYFHFHFGDKDKKIAPIETRRSIEVPLNERICLVGSGQSTNESEKPSILVEKICISPP 120

Qy 121 EGDPEAVTELCIWHNLSYMKCSWLPGRNTSPDNTYLYWHSLEKIHQENIFREGQ 180
| | | | |
Db 121 EGDPEAVTELCIWHNLSYMKCSWLPGRNTSPDNTYLYWHSLEKIHQENIFREGQ 180

Qy 181 YFGCSFDLTKVQSSFEQHSQIWKONAGKIKPSFNIVPLTSRVKDPDPPHINKLSFND 240
| | | | |
Db 181 YFGCSFDLTKVQSSFEQHSQIWKONAGKIKPSFNIVPLTSRVKDPDPPHINKLSFND 240

Qy 241 DLYVQWENPQNFISRLCFYEVVNNSTQTHNVFVYQBAKCNPEFERNVENTSCFMVPG 300
| | | | |
Db 241 DLYVQWENPQNFISRLCFYEVVNNSTQTHNVFVYQBAKCNPEFERNVENTSCFMVPG 300

Qy 301 VLPDNTLVIRVKTNKLCEYEDDKLWSNWSQEMTIGKRNSTLYITMLLIVPVIIVAGAI 360
| | | | |
Db 301 VLPDNTLVIRVKTNKLCEYEDDKLWSNWSQEMTIGKRNSTLYITMLLIVPVIIVAGAI 360

Qy 361 VLLLYLKLKLIIFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 420
| | | | |
Db 361 VLLLYLKLKLIIFPPIDPGKIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIE 420

Qy 421 LKASQ 426
| | | | |
Db 421 LKASQ 426

RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. US20020165135A1

; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 3; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.7e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

Qy 22 GGGGAPTETQPPVTNLVSVENLCTVIWNPPEGASSNCSLWYFHFHFGDKDKKIAPIET 81
| | | | |
Db 1 GGVAAPTETQPPVTNLVSVENLCTVIWNPPEGASSNCTLRYSFHFHFGDKDKKIAPIET 60

Qy 82 RRSIEVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDDPESAVTELCIWHNLSYM 141
| | | | |
Db 61 HRSKEVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDDPESAVTELCIWHNLSYM 120

Qy 142 KCSWLPGRNTSPDNTYLYWHSLEKIHQENIFREGQYFGCSFDLTKVQSSFEQHSV 201
| | | | |
Db 121 KCTWLPGRNTSPDNTYLYWHSLEKIHQENIFREGQYFGCSFDLTKVQSSFEQHSV 180

Qy 202 QIWKONAGKIKPSFNIVPLTSRVKDPDPPHINKLSFNDLIVQWENPQNFISRLCFYEV 261
| | | | |
Db 181 QIWKONARKIRPSFNIVPLTSRVKDPDPPHINKLFFQGNLYVQWENPQNFISRLCFYEV 240

Qy 262 EVNNSQTHNVFVYQBAKCNPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEY 321
| | | | |
Db 241 EVNNSQTHNVFVYQBAKCNPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEY 300

Qy 322 DDKLWSNWSQEMTIGKRNSTLYITMLLIVPVIIVAGAIIVLLYLRKLIIFPPIDPG 381
| | | | |
Db 301 DDKLWSNWSQEMTIGKRNSTLYITMLLIVPVIIVAGAIIVLLYLRKLIIFPPIDPG 360

Qy 382 KIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIEENLKASQ 426
| | | | |
Db 361 KIFKEMFGDQNDTLHWKKYDIYEKQKEETDSVVLIEENLKASQ 405

RESULT 6
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405

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; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-753-159-50

Query Match      80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.7e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 22 GGGGAPETOPPTNLSVSVENLCTVIWTPNPEGASSNCLWYFHFQDKQDKKIAPET 81
Db 1 GGVAAPTETOPPTNLSVSVENLCTVIWTPNPEGASPNCTLRYFHFQDKQDKKIAPET 60

QY 82 RRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKCSIPPEGDPESAVTELQCIWHNLSYM 141
Db 61 HRSKEVPLNERICLVQSGQCSSTNESONPSILVEKCTPPPEGDPESAVTELQCIWHNLSYM 120

QY 142 KCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVQDSFFQHSV 201
Db 121 KCTWLPGRNTSPDNTNLYYHRSLSGLKLOCEDIYREGQHIGCSFALTNLKDSFFQHSV 180

QY 202 QIMVKONAGIKPSFNIVPLTSRVKDDPPHINKLSFHNDLLYQWENPQNFISRCIFYEV 261
Db 181 QIMVKONARKIRPSFNIVPLTSRVKDDPPHINKLFFQGNLYYQWKNPQNFYSRCLSYQV 240

QY 262 EVNNSOTETHNVFVQEAKEENPEFERNVENTSCFMVPGVLPDPLTNTVIRVKTNKLCE 321
Db 241 EVNNSOTETNDIIFYBEAKCONSEFEGNLEGTCFMVPGVLPDPLTNTVIRVKTNKLCE 300

QY 322 DDKLSNWSQMSIGKRRNSTLVTMLLIVPVIAGAILVLLYLKRLKIIIPPIPDGP 381
Db 301 DDKLSNWSQMSIGENTDPTFTVITMLLATQVIVAGAILVLLYLKRLKIIIPPIPDGP 360

QY 382 KIPKEMFGQNDTLLHWKYDIYEKQKETSVDTSVLIENLKASQ 426
Db 361 KIPKEMFGQNDTLLHWKYDIYEKQKETSVDTSVLIENLKASQ 405

RESULT 7
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-34

Query Match      80.8%; Score 1875.5; DB 3; Length 780;
Best Local Similarity 99.4%; Pred. No. 6.6e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPPGASS 59
Db 1 MWPARGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASS 60

QY 60 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKCSIP 119
Db 61 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKCSIP 120

QY 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 180

QY 180 QYFGCSFDLTWKVQDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVQDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLVQWENPQNFISRCIFYEVVNNSTQETHNVFVQEAKEENPEFERNVENTSCFMVP 299
Db 241 DDLVQWENPQNFISRCIFYEVVNNSTQETHNVFVQEAKEENPEFERNVENTSCFMVP 300

QY 300 GVLPTDLTNTVIRVKTNKLCEYEDDKLSNWSQMSIGKRRNST 342
Db 301 GVLPTDLTNTVIRVKTNKLCEYEDDKLSNWSQMSIGKRRNST 343

RESULT 8
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match      80.8%; Score 1875.5; DB 3; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEWPARGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTPNPPGASS 59
Db 1 MWPARGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPGASS 60

QY 60 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKCSIP 119
Db 61 NCSLWYFHFQDKQDKKIAPETRRSIEVPLNERICLVQSGQCSSTNESEKPSILVEKCSIP 120

QY 120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDNTNLYYHRSLEKIHOCENIFREG 180

QY 180 QYFGCSFDLTWKVQDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHN 239
Db 181 QYFGCSFDLTWKVQDSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLVQWENPQNFISRCIFYEVVNNSTQETHNVFVQEAKEENPEFERNVENTSCFMVP 299
Db 241 DDLVQWENPQNFISRCIFYEVVNNSTQETHNVFVQEAKEENPEFERNVENTSCFMVP 300

QY 300 GVLPTDLTNTVIRVKTNKLCEYEDDKLSNWSQMSIGKRRNST 342
Db 301 GVLPTDLTNTVIRVKTNKLCEYEDDKLSNWSQMSIGKRRNST 343

RESULT 9
US-09-935-868-32
; Sequence 32, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
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; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-32

Query Match      80.8%; Score 1875.5; DB 3; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 300
QY 300 GVLPTLTNTVRIKVTNKLCEYDDKLSNWSQEMSIGKGRNST 342
Db 301 GVLPTLTNTVRIKVTNKLCEYDDKLSNWSQEMSIGKGRNST 343

RESULT 11
US-10-282-162-32
; Sequence 32, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGNERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

Query Match      80.8%; Score 1875.5; DB 4; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 300

Query Match      80.8%; Score 1875.5; DB 4; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 119
Db 61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLOVGSQCSTNESEKPSILVEKICIS 120
QY 120 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 179
Db 121 PEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYTLYYWHSLEKIHOCENIFREG 180
QY 180 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 239
Db 181 QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPDPPHIKNLSFHN 240
QY 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECENPEFERNVENTSCFMVP 300
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QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 343

RESULT 12

US-11-134-114-32
; Sequence 32, Application US/111134114
; Publication No. US20050222033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203CI
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-32

Query Match 80.8%; Score 1875.5; DB 6; Length 793;
Best Local Similarity 99.4%; Pred. No. 6.8e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179
Db 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 180
QY 180 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPPHKNLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPPHKNLSFHN 240
QY 240 DDLYQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAACENPFRNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 343

RESULT 13

US-09-935-868-42
; Sequence 42, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-42

Query Match 80.5%; Score 1866.5; DB 3; Length 780;
Best Local Similarity 99.1%; Pred. No. 3.9e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179
Db 121 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 180
QY 180 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPPHKNLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPPHKNLSFHN 240
QY 240 DDLYQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAACENPFRNVENTSCFMVP 299
Db 241 DDLYQWENPQNFISRCLFYEVEVNNSTQETHNVFVQEAACENPFRNVENTSCFMVP 300
QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKKRNST 343

RESULT 14

US-09-935-868-48
; Sequence 48, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-48

Query Match 80.5%; Score 1866.5; DB 3; Length 782;
Best Local Similarity 99.1%; Pred. No. 3.9e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MWPARLCGLWALLLCAGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 59
Db 1 MWPARLCGLWALLLCAGGGGGGAAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS 60
QY 60 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 119
Db 61 NCSLWYFSHFQDKQDKKIAPETRRSIEVPLNERICIQVGSQCSTNSEKPSILVEKICIS 120
QY 120 PEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYTYWHRSLKIHQOCENIFREG 179

Db 121 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQCENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPPIKNLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPPIKNLSFHN 240
Qy 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECFERNVENTSCFMVP 300
Qy 300 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 343

RESULT 15
US-09-935-868-38
; Sequence 38, Application US/09935868
; Patent No. US2002016490A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-935-868-38

Query Match : 80.4%; Score 1865.5; DB 3; Length 780;
Best Local Similarity 99.1%; Pred. No. 4.7e-150;
Matches 340; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MEWPARLCGLWALLCAGGGGGGGG-APTETOPPTNLSVSVENLCTVIWNPPEGASS 59
Db 1 MYWPARLCGLWALLCAGGGGGGAAPTETQPTNLSVSVENLSTVIWNPPEGASS 60
Qy 60 NCSLWYFSGDKDKKIAPETERISIEVPLNERICLVGSCQSTNESEKPSILVEKCI 119
Db 61 NCSLWYFSGDKDKKIAPETERISIEVPLNERICLVGSCQSTNESEKPSILVEKCI 120
Qy 120 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQCENIFREG 179
Db 121 PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQCENIFREG 180
Qy 180 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPPIKNLSFHN 239
Db 181 QYFGCSFDLTWKVDSSFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKDPDPPIKNLSFHN 240
Qy 240 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECFERNVENTSCFMVP 299
Db 241 DDLYVQWENPQNFISRCIFYEVEVNNSTETHNVFYVQEAKECFERNVENTSCFMVP 300
Qy 300 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 342
Db 301 GVLPTLTNTVIRVKTINKLCYEDDDKLSNWSQEMSIGKKRNST 343

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 ; Search time 9.28509 Seconds
(without alignments)
602.062 Million cell updates/sec

Title: US-10-036-568A-4
Perfect score: 2320
Sequence: 1 MEMPALCGLWALLCAGGG.....OTKETDSVLIENLKASQ 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No! is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2309.5	99.5	427	US-11-185-230-4	Sequence 4, Appli
2	1687	72.7	424	US-11-185-230-6	Sequence 6, Appli
3	296.5	12.8	420	US-11-185-230-5	Sequence 5, Appli
4	294.5	12.7	380	US-10-989-313-4	Sequence 4, Appli
5	294.5	12.7	380	US-11-185-230-2	Sequence 2, Appli
6	293.5	12.7	378	US/11/185	Sequence 12, Appli
7	287.5	12.4	383	US-10-989-313-2	Sequence 2, Appli
8	230	9.9	313	US-11-193-512-106	Sequence 106, App
9	202	8.7	341	US-10-511-722-21	Sequence 21, Appli
10	202	8.7	357	US-10-511-722-20	Sequence 20, Appli
11	202	8.7	369	US-11-105-268-60	Sequence 60, Appli
12	178.5	7.7	411	US-11-075-351-47	Sequence 47, Appli
13	173	7.5	646	US-10-995-561-695	Sequence 695, App
14	173	7.5	708	US-10-636-320-2	Sequence 2, Appli
15	173	7.5	918	US-10-995-561-696	Sequence 696, App
16	168.5	7.3	329	US-10-995-561-694	Sequence 694, App
17	168	7.2	897	US-11-124-367A-449	Sequence 449, App
18	168	7.2	897	US-11-124-367A-451	Sequence 451, App
19	166	7.2	903	US-11-124-367A-450	Sequence 450, App
20	125	5.4	825	US-10-995-561-679	Sequence 679, App
21	125	5.4	825	US-11-124-367A-469	Sequence 469, App
22	125	5.4	852	US-11-104-923A-5	Sequence 5, Appli
23	118	5.1	521	US-11-105-268-58	Sequence 58, Appli
24	113	4.9	631	US-10-813-646-22	Sequence 22, Appli
25	111.5	4.8	979	US-10-636-320-6	Sequence 6, Appli

26	107.5	4.6	360	7	US-11-084-408-3	Sequence 3, Appli
27	106	4.6	589	6	US-10-821-234-1687	Sequence 1687, Ap
28	105	4.5	529	7	US-11-132-947-8	Sequence 8, Appli
29	102.5	4.4	1905	6	US-10-877-346-44	Sequence 44, Appli
30	101.5	4.4	896	7	US-11-192-219-3	Sequence 3, Appli
31	101.5	4.4	898	7	US-11-166-730-3	Sequence 3, Appli
32	101.5	4.4	923	7	US-11-192-219-4	Sequence 4, Appli
33	101.5	4.4	1165	7	US-11-192-219-2	Sequence 2, Appli
34	100.5	4.3	2214	7	US-11-080-991-94	Sequence 94, Appli
35	97	4.2	1368	6	US-10-995-561-539	Sequence 539, App
36	96.5	4.2	984	7	US-11-113-424-60	Sequence 60, Appli
37	96	4.1	783	7	US-11-192-219-7	Sequence 7, Appli
38	95.5	4.1	1433	7	US-11-094-519A-40	Sequence 40, Appli
39	95	4.1	551	7	US-11-022-289-7	Sequence 7, Appli
40	95	4.1	1178	7	US-11-044-899-29	Sequence 29, Appli
41	94	4.1	1711	7	US-11-143-984A-38	Sequence 38, Appli
42	93.5	4.0	836	6	US-10-821-234-1559	Sequence 1559, Ap
43	92.5	4.0	983	7	US-11-113-424-59	Sequence 59, Appli
44	92	4.0	557	7	US-11-022-289-2	Sequence 2, Appli
45	92	4.0	557	7	US-11-022-289-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: INV924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match	99.5%;	Score	2309.5;	DB	7;	Length	427;		
Best Local Similarity	99.8%;	Pred. No.	1.3e-196;						
Matches	426;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
Qy	1	MEMPALCGLWALLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS	59						
Db	1	MEMPALCGLWALLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS	60						
Qy	60	NCSLWYFHFHFGDKDKKTAPEPTRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCI	119						
Db	61	NCSLWYFHFHFGDKDKKTAPEPTRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCI	120						
Qy	120	PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQCNIFREG	179						
Db	121	PEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQCNIFREG	180						
Qy	180	QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPHINKNLSFHN	239						
Db	181	QYFGCSFDLTVKVDSSEFEQHSVQIMVKDNAGIKPSFNIVPLTSRVKPPDPHINKNLSFHN	240						
Qy	240	DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQAEKCNPEFRNVENTSCFMPV	299						
Db	241	DDLYVQWENPQNFISRCIFYEVEVNNNSQTEHNVFYQAEKCNPEFRNVENTSCFMPV	300						

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QY 300 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 359
DB 301 GVLPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
QY 360 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYERQTKETDSVVLIE 419
DB 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYERQTKETDSVVLIE 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427
RESULT 2
US-11-185-230-6
; Sequence 6, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT 3
; ORGANISM: Mus musculus
; FEATURE:
US-11-185-230-6
Query Match 72.7%; Score 1687; DB 7; Length 424;
Best Local Similarity 74.6%; Pred. No. 1.3e-141;
Matches 317; Conservative 40; Mismatches 66; Indels 2; Gaps 2;
QY 1 MEWPARLCGLWALLCAGGGGGGAPTETQPPVTNLSVSNLCTVITWNPPEGASSN 60
DB 1 MARPALLGELLVLLWTATVGVAAA-TEVQPPVTNLSVSNLCTVITWNPPEGASSN 59
QY 61 CSLWYFHFHGDQDKKIAPETRHSIEVPLNERICLVGSGCSTNESEKPSILVEKICISPP 120
DB 60 CTLRYFHFHFDQDKKIAPETRHRKEELPLDEKICLVGSGCSANESSEKPSPLVKKICISPP 119
QY 121 EGDPESAVTELOCITWHLNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQ 180
DB 120 EGDRESAVTELCITWHLNLSYMKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFREGQ 179
QY 181 YFGCSPLDTVKDSSPEHSHQVIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFND 240
DB 180 HIACSFALTKV-BPSFHHQVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFND 238
QY 241 DLXVQWENPQNFISRCLEFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVPG 300
DB 239 ALLVQWKNPQNFISRCLEFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVPG 298
QY 301 VLPDPTLTNTVIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 360
DB 299 VLADAVYTVRVRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAI 358
QY 361 VLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYERQTKETDSVVLIE 420
DB 359 ILFLYLRKLIIFPPIDPGKIFKEMFGDQNDTTLHWKKYDIYERQTKETDSVVLIE 418
QY 421 LKXAS 425
DB 419 LKXAA 423
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```
RESULT 3
US-11-185-230-5
; Sequence 5, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 420
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-5
Query Match 12.8%; Score 296.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 9.3e-19;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;
QY 32 PPVTNLSVSNLCTVITWNP-PEGASSNCSLWYFHFHGDQDKKIAPETRHSIEVPLN 90
DB 32 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVLLEY-----QVKINAPK-EDDYETRI 82
QY 91 ERICLVQ-----GSCQSTNESEKPSILVEKICIS-----PPEGDPESAVTELOCITWHLN 138
DB 83 ESKCVTLILHKGPSASVRTILQNDHSLASSWASAEHLHAPGPSPTSVNLCTTNTTETDN 142
QY 139 -----SY-----MKCSWLPGRNTSPDTNTLYYHRSLEKIHQENIFRE--QYFEGCSFDL 188
DB 143 YSLRSLYQVSLHCTWLVGTDAEDTQYFLYRYGSWTE--ECQFYSKDTLGRNIACWFFR 200
QY 189 TKVKDSSFEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNDLXVQWEN 248
DB 201 TFLSKGRDWLSVLVNGSKHSIRFPDQLFALHAIDQINPLNVTAEIEGTRLSIQWEK 260
QY 249 PQN-FISRCLEFYEVEVNNSTQTHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLN 307
DB 261 PVSAFPIHCFDYEVKIHNTNG-----YLQIEKLTNAFTSIIDLSKY----- 304
QY 308 TVRIRVKTNKLCEYDDKLSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLK 367
DB 305 DVQVRAAVSSMCREAG-LMSNSQPIYVGNDEHKPLREWFVIVIMATICIFILILSLICK 363
QY 368 --RLKIIIPPIPDGKIFKEMFGDQNDTTLHWKKYDIYERQTKETDSVVL 417
DB 364 ICHLWIKLPPPIAPKSNIKDLFTVTN-----YEKAGSSETEIEVI 404
RESULT 4
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
```

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; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-989-313-4

Query Match      12.7%; Score 294.5; DB 6; Length 380;
Best Local Similarity 27.0%; Pred. No. 1.2e-18;
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;

Qy 51 WNPPEGAS--SNCSLWYFSHFHFGDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHPKECTVEY-----ELKYRNIGSETWKTIIITKNLHYKDGFDLKNKGIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDPDESATVTELOCIWHNLSYMKCSWLPGRWNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PGIPETKVQDMDCVYVNWQYLLCSWKPGIGVLL 165

Qy 154 DTNTLYYWHRSLEKIHQC--ENIPREGQVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNLYFYWEGDLHALQCVDIYKADQNGICRFFYLEASD--YKDFYICVNGSSSENKPI 223

Qy 213 KPSFNIVPLTSRVKPPPHIKNLSFHN-----DLVYQWENPQNF1--SRCLFYEVENVNSQT 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWKSIPGLPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLKTTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPPIDP 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFIILIVFVTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFPFCD 379

RESULT 5
US-11-185-230-2
; Sequence 2, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11/185,230-12

Query Match      12.7%; Score 293.5; DB 7; Length 378;
Best Local Similarity 27.5%; Pred. No. 1.5e-18;
Matches 94; Conservative 55; Mismatches 130; Indels 63; Gaps 18;

Qy 51 WNPPEGAS--SNCSLWYFSHFHFGDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHPKECTVEY-----ELKYRNIGSETWKTIIITKNLHYKDGFDLKNKGIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDPDESATVTELOCIWHNLSYMKCSWLPGRWNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PGIPETKVQDMDCVYVNWQYLLCSWKPGIGVLL 165

Qy 154 DTNTLYYWHRSLEKIHQC--ENIPREGQVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNLYFYWEGDLHALQCVDIYKADQNGICRFFYLEASD--YKDFYICVNGSSSENKPI 223

Qy 213 KPSFNIVPLTSRVKPPPHIKNLSFHN-----DLVYQWENPQNF1--SRCLFYEVENVNSQT 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWKSIPGLPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLKTTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPPIDP 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFIILIVFVTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFPFCD 379

RESULT 6
US/11/185
; Sequence 12, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 378
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11/185,230-12

Query Match      12.7%; Score 294.5; DB 7; Length 380;
Best Local Similarity 27.0%; Pred. No. 1.2e-18;
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;

Qy 51 WNPPEGAS--SNCSLWYFSHFHFGDKQDKKIAPETRISI-----EVLNERICLQVGS 99
Db 53 WQPLSLDHPKECTVEY-----ELKYRNIGSETWKTIIITKNLHYKDGFDLKNKGIEAKIHT 107

Qy 100 -----QCSNTESEKPSILVEKC--ISPPGDPDESATVTELOCIWHNLSYMKCSWLPGRWNTSP 153
Db 108 LLPWQC--TNGSEVQSSWAETTYWIS--PGIPETKVQDMDCVYVNWQYLLCSWKPGIGVLL 165

Qy 154 DTNTLYYWHRSLEKIHQC--ENIPREGQVFGSPDLTKVKDSSFEQHSVQIMVKDNAGKI 212
Db 166 DTNLYFYWEGDLHALQCVDIYKADQNGICRFFYLEASD--YKDFYICVNGSSSENKPI 223

Qy 213 KPSFNIVPLTSRVKPPPHIKNLSFHN-----DLVYQWENPQNF1--SRCLFYEVENVNSQT 268
Db 224 RSYFTFQQLQNVKPLPP--VYLTFRESSCEIKLWKSIPGLPIPARCFDYEIREDDT 281

Qy 269 ETHNVFYVQEAECNPEFERNVENTS---CFMVGVLPTLNTVIRVKTNKLVCYEDDKL 325
Db 282 T-----LVTATVENETYLKTTNETRQLCFV-----RSKVNIIYC--SDGI 321

Qy 326 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKLIIPPPIDP 380
Db 322 WSESDKQCEGEGDLSKTLRFLWLPF-----GFIILIVFVTGL--LLRKPNTYP 370

Qy 381 GKIFKEMFGD 390
Db 371 -KMIPFPFCD 379

RESULT 5
US-11-185-230-2
; Sequence 2, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted
US/11-185-230-2

Query Match      12.7%; Score 294.5; DB 7; Length 380;
Best Local Similarity 27.0%; Pred. No. 1.2e-18;
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;
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Qy 269 ETHNVFVQAKCENPEFERNVENTS---CFMVPGLVPLDTLNTVIRVTKNKLCEYDDKL 325
Db 282 T-----LVTATVENETITLKTNETKQLCFV-----RSKVNIIYC-SDGII 321
Qy 326 WSNWSQBM-----SIGKRNSTLYIT--MLLIYPVIVAGAIL 360
Db 322 WSEWSKQCEGEDLSKTLRLFWLPGFILLIVFTVGLLL 363

RESULT 7

US-10-989-313-2
; Sequence 2, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Maresha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-989-313-2

Query Match 12.4%; Score 287.5; DB 6; Length 383;
Best Local Similarity 25.6%; Pred. No. 5.2e-18;
Matches 89; Conservative 54; Mismatches 156; Indels 49; Gaps 14;
Qy 51 WNP-----EGASSNCSLWYFSGDKQDKIAPETRRSIEVPLNE---RCLQVGSQ 100
Db 47 WKPVVIEKFGCTLEYELKYRNVDSWKTITRLNIYKQFDLKNLGEKIRTHLSEH 106
Qy 101 CSTNESEKPSILVEKCI--PPEGDPESAVTELCIWHNLSYMKCSWLPGRNTSPDNTYL 159
Db 107 C-TNGSEVQSPWIEASVIGSDEGSLETKIQDMKCIYNYWQYLVCSMKPGKTVVSDNTYTM 165
Qy 160 YYHRSLEKIHQENIFR-BGQYFGSGFDLTWKVDSSEFQHSVQIMVKDNAGKIKPSFNI 218
Db 166 FFWEYEGIDHALQCADYLOHDERKNVGCK--LSNLDSSDYKDPFFICVNGSSKLEPIRSSYTV 223
Qy 219 VPLTSRVKPPPHIKNLSFHND-DLVYQWENPQNF1-SRCLFYEVEVNNNSQTETHNVFV 276
Db 224 FQONIVKPLPPFLHLSVENSIDRMKSTPGGPIPPRCYTYEIVREDDISWEGATDK 283
Qy 277 QEAKCENPEFERNVENTSCFMVPGLVPLDTLNTVIRVTKNKLCEYDDKLWNNWSQEMS-- 334
Db 284 NDMKLR--RANESEDLCPFV-----RCKVNIYC-ADGGINSESESECWE 326
Qy 335 --IGKRNSTLYITMLLIYPVIVAGAILVLLYLKRLKIIFPPIDP 380
Db 327 GYTGPDSK-----IIPVIVPCLFFIFLLLLCL-----IVEKEEPEP 363

RESULT 8

US-11-193-512-106
; Sequence 106, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, Nobuo
; TAKATSU, Kiyoshi
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5 Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-Aug-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-11-193-512-106
Query Match 9.9%; Score 230; DB 7; Length 313;
Best Local Similarity 24.8%; Pred. No. 4.8e-13;
Matches 82; Conservative 51; Mismatches 145; Indels 52; Gaps 14;
Qy 32 PPVTNLSVSVENICTVIWTWNP--PEGASSNCSLWYFSGDKQDKIAPETRRSIEVPLN 90
Db 12 PPV-NTFIKVTGLAQVLLQWKNPDQEQRNVLEY-----QVKINAPK-EDYETRI 62
Qy 91 ERICLQV-----GSGCSTNESEKPSILVEKCI--PPEGDPESAVTELCIWHNLS--- 138
Db 63 ESKCVTLHKFGFSASVRTILQNDHSLASSASAEHLHAPGSPGTSVNLTCITTTEDN 122
Qy 139 -----SY-----MKCSWLPGRNTSPDNTYLYHRSLEKIHQENIFR--GQYFGSGFDL 188
Db 123 YSLRSYQVSLHCTLVGTDAEDTQYFLYRYGSWTE--EQEYSKDTLGRNIACWPPR 180
Qy 189 TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIPLTSRVKPPPHIKNLSFNDLIVYQWEN 248
Db 181 TFIILSKGRDLAVLVNGSSKHSNAIRFDQIFALHAIQINPPLNVTAEIGTSLSQWEK 240
Qy 249 PQN-FISRCLFYEVEVNNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGLVPLDTLN 307
Db 241 PVSAPFIHCFDVEVKHTNRNG-----YLQIEKLMTNATFISIDDLISKY----- 284

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-722-20

Query Match      8.7%; Score 202; DB 6; Length 357;
Best Local Similarity 27.2%; Pred. No. 1.7e-10;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

Qy 130 ELQCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSI--EKIHQCN-IFREGQYFGCSF 186
Db 59 EVQCFVFNVEYMNCTWNSSEPPQ-TNLTLHYWYKNSDNKVKQKSHYLFSEITSGC-- 115
Qy 187 DLTKVKDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPPHIKNLSFH---NDLLY 243
Db 116 QLOKKEIHLYQTFVVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQLE 171
Qy 244 WOMENPQNFISRL-----FYEVVNSQTEHNVFYVQEAECENPEFERNVENTSCFVMP 299
Db 172 LWNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSDYRHKFSLP 211
Qy 300 GVLPTLNTVIRVKTNKLCEYDDKLGNSWQSEMSIG---KKNSTLYITMLLIVPVIVA 356
Db 212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSWSHPHIGWSNTSKENPFLFALEAVVISVGS 270
Qy 357 GAIIVLL---LYLKRLLKIIIPPIP 378
Db 271 GLIISLLCVFWLER----TMPRIIP 291

RESULT 11
US-11-105-268-60
; Sequence 60, Application US/11105268
; Publication No. US200502604A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; PRIOR FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-60

Query Match      8.7%; Score 202; DB 7; Length 369;
Best Local Similarity 27.2%; Pred. No. 1.8e-10;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

Qy 130 ELQCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSI--EKIHQCN-IFREGQYFGCSF 186
Db 59 EVQCFVFNVEYMNCTWNSSEPPQ-TNLTLHYWYKNSDNKVKQKSHYLFSEITSGC-- 115
Qy 187 DLTKVKDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPPHIKNLSFH---NDLLY 243
Db 116 QLOKKEIHLYQTFVVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQLE 171
Qy 244 WOMENPQNFISRL-----FYEVVNSQTEHNVFYVQEAECENPEFERNVENTSCFVMP 299
Db 172 LWNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSDYRHKFSLP 211
Qy 300 GVLPTLNTVIRVKTNKLCEYDDKLGNSWQSEMSIG---KKNSTLYITMLLIVPVIVA 356
Db 212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSWSHPHIGWSNTSKENPFLFALEAVVISVGS 270
Qy 357 GAIIVLL---LYLKRLLKIIIPPIP 378
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Qy 308 TVRIRVKTNKLCEYDDKLGNSWQSEMSIGK 337
Db 285 DVQRAAVSMCREAG-LWSEWSQPIYVGK 313

RESULT 9
US-10-511-722-21
; Sequence 21, Application US/10511722
; Publication No. US20050287144A1
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd.
; APPLICANT: Wallach, David
; APPLICANT: Shmushkovich, Taisia
; APPLICANT: Ramakrishnan, Parameswaran
; TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation a
; FILE REFERENCE: 530
; CURRENT APPLICATION NUMBER: US/10/511,722
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 149217
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 152183
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-722-21

Query Match      8.7%; Score 202; DB 6; Length 341;
Best Local Similarity 27.2%; Pred. No. 1.6e-10;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;

Qy 130 ELQCIWHNLSYMKCSWLPGRNTSPDNTYLYYHRSI--EKIHQCN-IFREGQYFGCSF 186
Db 59 EVQCFVFNVEYMNCTWNSSEPPQ-TNLTLHYWYKNSDNKVKQKSHYLFSEITSGC-- 115
Qy 187 DLTKVKDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPPHIKNLSFH---NDLLY 243
Db 116 QLOKKEIHLYQTFVVQL--QDPREPRQATQMLKQLNVLVWPAP--ENLTLKLSQLE 171
Qy 244 WOMENPQNFISRL-----FYEVVNSQTEHNVFYVQEAECENPEFERNVENTSCFVMP 299
Db 172 LWNWN--RFLNHCLEHLVQYRTDWDHWT-----EQSDYRHKFSLP 211
Qy 300 GVLPTLNTVIRVKTNKLCEYDDKLGNSWQSEMSIG---KKNSTLYITMLLIVPVIVA 356
Db 212 SVDGQKRYTFRVRSRFPNPLC-GSAQHWSWSHPHIGWSNTSKENPFLFALEAVVISVGS 270
Qy 357 GAIIVLL---LYLKRLLKIIIPPIP 378
Db 271 GLIISLLCVFWLER----TMPRIIP 291

RESULT 10
US-10-511-722-20
; Sequence 20, Application US/10511722
; Publication No. US20050287144A1
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd.
; APPLICANT: Wallach, David
; APPLICANT: Shmushkovich, Taisia
; APPLICANT: Ramakrishnan, Parameswaran
; TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation a
; FILE REFERENCE: 530
; CURRENT APPLICATION NUMBER: US/10/511,722
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 149217
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 152183
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 21
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```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 708 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-636-320-2

Query Match      7.5%; Score 173; DB 6; Length 708;
Best Local Similarity 25.0%; Pred. No. 1.5e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;

Qy 31 QPVTNLSVSVENLCTVIWTPWPPGASSNCSLWYFHFHG-DKQDKKIAPETRRSIEVPL 89
Db 34 ESPVQLHSNFTAVCVLKEKCMDFHVNANIVWKNHTIPREQYTIINRTASSVTFTD 93

Qy 90 NERICLVGSCSTNBEKPSILVEKCIS--PPEGDPESAVTELCQIWHNLSYMKCSWLP 147
Db 94 IASLNIQLTCNLTGQLEQNVYGITIISGLPPE-KPKN----LSCI VNEGKKWRCWDG 148

Qy 148 GRNTSPDNTYTL-YYWHRSLKIHQENIFREGQYFGCSFDLTKVKDSSPEQHSVQIMVK 206
Db 149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201

Qy 207 DNAGKI-KPSFNIVPLTSRVKPPPHIKNLSFHND-----LYQWENPQNFISRCIFYE 260
Db 202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEELSSILKLTWNPISIKSVIILKYN 258

Qy 261 VEVNSQTETHNVFVQAEKCNPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKLKY 320
Db 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPTEYVFRIR-----CM 302

Qy 321 EDD--KLMSNWSQEMS--IGKRNSTLYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPP 376
Db 303 KEDGKGYSWDSERASGITTYEDRPSKAPSWYKIDPSHTQGYRTVQLVW-KTL-----PP 356

Qy 377 IPDPGKIPKEMFGDNDTLHWKDYIEKQTKETSDSVLIEN 420
Db 357 FEANGKIL-----DYEVTLTRWKS--LQNYTVNATKLTVNLTN 393

RESULT 15
US-10-995-561-696
; Sequence 696, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-696

Query Match      7.5%; Score 173; DB 6; Length 918;
Best Local Similarity 25.0%; Pred. No. 2e-07;
Matches 101; Conservative 51; Mismatches 194; Indels 58; Gaps 21;

Qy 31 QPVTNLSVSVENLCTVIWTPWPPGASSNCSLWYFHFHG-DKQDKKIAPETRRSIEVPL 89
Db 34 ESPVQLHSNFTAVCVLKEKCMDFHVNANIVWKNHTIPREQYTIINRTASSVTFTD 93

Qy 90 NERICLVGSCSTNBEKPSILVEKCIS--PPEGDPESAVTELCQIWHNLSYMKCSWLP 147
Db 94 IASLNIQLTCNLTGQLEQNVYGITIISGLPPE-KPKN----LSCI VNEGKKWRCWDG 148
```

```
Qy 148 GRNTSPDNTYTL-YYWHRSLKIHQENIFREGQYFGCSFDLTKVKDSSPEQHSVQIMVK 206
Db 149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201

Qy 207 DNAGKI-KPSFNIVPLTSRVKPPPHIKNLSFHND-----LYQWENPQNFISRCIFYE 260
Db 202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEELSSILKLTWNPISIKSVIILKYN 258

Qy 261 VEVNSQTETHNVFVQAEKCNPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKLKY 320
Db 259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPTEYVFRIR-----CM 302

Qy 321 EDD--KLMSNWSQEMS--IGKRNSTLYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPP 376
Db 303 KEDGKGYSWDSERASGITTYEDRPSKAPSWYKIDPSHTQGYRTVQLVW-KTL-----PP 356

Qy 377 IPDPGKIPKEMFGDNDTLHWKDYIEKQTKETSDSVLIEN 420
Db 357 FEANGKIL-----DYEVTLTRWKS--LQNYTVNATKLTVNLTN 393
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Job time : 10.2851 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 ; Search time 98.483 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345
Perfect score: 1760
Sequence: 1 APTTQPPVNLVSVENLCL.....WSNWSQEMSGCKKSTLYI 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1760	100.0	414	ADX97531	Pancreati
2	1760	100.0	426	AAW09822	Human int
3	1760	100.0	427	AAW24973	Human int
4	1760	100.0	427	AAW19807	Human int
5	1760	100.0	427	ADFL7835	Human IL-
6	1760	100.0	427	ADFL71812	Human int
7	1760	100.0	427	ADFL71814	Human int
8	1760	100.0	427	ADL82843	Human PRO
9	1760	100.0	427	ADN04504	Antipsori
10	1760	100.0	427	ADN62575	Human int
11	1760	100.0	427	ABM82441	Tumour-as
12	1754	99.7	427	AAW19808	Human int
13	1754	99.7	427	ADFL71813	Human int
14	1745	99.1	322	AAE13745	Human sol
15	1745	99.1	664	ADFL7841	Chimeric
16	1745	99.1	784	AAW92207	IL-13/IL-
17	1745	99.1	784	ABW02180	Human IL-
18	1745	99.1	793	AAW92208	IL-13/IL-
19	1745	99.1	793	ABW02181	Human IL-
20	1478	84.0	405	AAW69132	Canine in
21	1324	75.2	426	AAW09821	Mouse int
22	1314	74.7	424	AAW97888	Marine IL
23	1124	63.9	286	AAW90678	Human DAL
24	773	43.9	177	AAW58987	Homo sapi

25	296	16.8	318	4	AAU69137	Canine IL
26	296	16.8	365	4	AAU69136	Canine in
27	296	16.8	386	4	AAU69135	Canine in
28	296	16.8	561	4	AAU69138	Canine IL
29	296	16.8	561	4	AAU69141	Canine IL
30	296	16.8	563	4	AAU69140	Canine IL
31	296	16.8	565	4	AAU69139	Canine IL
32	289	16.4	372	2	AAW36616	Celebus m
33	287	16.3	82	8	ADO26844	Human rec
34	284	16.1	310	8	ADS75553	IL13-R-al
35	284	16.1	315	2	AAW56261	Mature in
36	284	16.1	317	5	AAW13746	Human sol
37	284	16.1	359	2	AAW56260	Construct
38	284	16.1	380	2	AAW36613	Human Zcy
39	284	16.1	380	2	AAW35295	Human IL-
40	284	16.1	380	2	AAW24972	Human int
41	284	16.1	380	2	AAW33603	Homo sapi
42	284	16.1	380	2	AAW41502	Human cyt
43	284	16.1	380	2	AAW41520	Human HR-
44	284	16.1	380	3	AAW95296	IL-13 bin
45	284	16.1	380	4	AAW63812	Amino aci

ALIGNMENTS

RESULT 1
ADX97531
ID ADX97531 standard; protein; 414 AA.
XX
AC ADX97531;
XX
DT 21-APR-2005 (first entry)
XX
DE Pancreatic cancer associated human protein, SEQ ID 79.
XX
KW pancreas tumor; cytostatic.
XX
OS Homo sapiens.
XX
PN EPI471075-A2.
XX
PD 27-OCT-2004.
XX
PF 31-MAR-2004; 2004EP-00090124.
XX
PR 31-MAR-2003; 2003DE-01015834.
XX
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
PI Rosenthal A, Pilarisky C, Dahl E, Specht T, Bruemendorf T;
PI Lichtner R, Staub E, Roepcke S, Li X;
DR WPI; 2004-768082/76.
DR N-PSDB; ADX97460.
PT New nucleic acid differentially expressed in pancreatic tumor tissue, for
PT use as diagnostic agents and in screening for therapeutic agents.
PS Claim 2; SEQ ID NO 79; 28pp; German.
XX The invention relates to a novel human nucleic acid sequence of the
CC pancreas and its encoded protein. The invention further comprises:
CC proteins and peptides, preferably isolated, that contain a sequence
CC encoded by the novel nucleic acid; and methods for diagnosis and
CC treatment of pancreatic cancer, using a substance that inhibits or binds
CC to the protein or its DNA, including: an antisense oligonucleotide, short
CC interfering RNA or ribozyme directed against the pancreatic protein, an

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CC organic molecule, particularly having a molecular weight below 5000,
CC especially 300, that binds to the pancreatic DNA, an aptamer or
CC (monoclonal) antibody, preferably human or humanized, that binds to the
CC pancreatic DNA, or an anti-idiotypic antibody raised against the
CC monoclonal antibody, any of which may be derivatized with a reporter
CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
CC human pancreatic proteins and their encoding DNA have cytostatic
CC activity. The novel sequences are useful for inhibiting transcription
CC and/or expression of genes and proteins associated with pancreatic
CC cancer. This sequence represents one of the novel human pancreatic
CC proteins of the invention. Note: This sequence is not shown in the
CC specification, it has been electronically downloaded from a DVD-rom
CC provided with this specification by the European Patent Office.
XX
XX
SQ Sequence 414 AA;
Query Match 100.0%; Score 1760; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 3.9e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRRI 60
Db 14 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRRI 73
QY 61 EVPLNERICLVQGSQCSNTESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 120
Db 74 EVPLNERICLVQGSQCSNTESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 133
QY 121 LQGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 180
Db 134 LQGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 193
QY 181 KDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCLFYVEVNN 240
Db 194 KDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCLFYVEVNN 253
QY 241 SQTETHNVFYQBAKCNPFERNVENTSCFMVPGVLPDNLTVIRVKTNKLCEYDDKL 300
Db 254 SQTETHNVFYQBAKCNPFERNVENTSCFMVPGVLPDNLTVIRVKTNKLCEYDDKL 313
QY 301 WSNWSQEMSIGKKRNSTLYI 320
Db 314 WSNWSQEMSIGKKRNSTLYI 333
RESULT 2
AAW09822
ID AAW09822 standard; protein; 426 AA.
XX
XX AAW09822;
AC
DT 15-JUL-1997 (first entry)
XX
XX Human interleukin-12 receptor alpha chain NR4.
XX
XX NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine;
KW allergy; asthma; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= Sig_peptide
FT Protein 28..426
FT /label= Mat_protein
FT Domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT Modified-site 36
FT /label= N-glycosylation site
FT Modified-site 104
FT /label= N-glycosylation_site
FT Domain 119..342
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FT Modified-site 137
FT /label= Haemoreceptor_receptor-domain
FT Region 326..330
FT /label= N-glycosylation site
FT Domain 343..366
FT /label= WSDWS_motif
FT Domain 367..426
FT /label= Transmembrane_domain
FT /label= Cytoplasmic_tail
XX
XX W09715663-A1.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 23-OCT-1996; 96WO-AU000668.
PF
XX
XX 23-OCT-1995; 95AU-00006135.
PR
XX
XX 22-DEC-1995; 95AU-00007276.
PR
XX
XX 09-SEP-1996; 96AU-00002208.
PR
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX
XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
PI
XX
XX WPI; 1997-259018/23.
DR
XX
XX N-PSDB; AA166165.
DR
XX
XX DNA encoding animal haemopoietin receptor which interacts with
FT interleukin-13 - useful to treat asthma, allergy or condition exacerbated
FT by IgE production.
PT
XX
XX Claim 5; Page 52-54; 93pp; English.
PS
XX
XX Novel mouse and human haemoprotein receptors (AAW09822 and AAW09822),
CC designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
CC The human NR4 amino acid sequence was deduced from a composite DNA
CC sequence (AA166165) derived from bone marrow cDNA clones. Recombinant
CC NR4, or fusion proteins including NR4, can be produced in transformed
CC host cells. The receptor molecules and their components are useful in the
CC development of a range of agonists, antagonists, therapeutics and
CC diagnostic reagents based on ligand interaction with its receptor, esp.
CC for the development of cpds. capable of modulating the activity of IL-13
CC and related cytokines such as interleukin-4 for the treatment of allergy,
CC asthma and other conditions relating to IgE
XX
XX
SQ Sequence 426 AA;
Query Match 100.0%; Score 1760; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRRI 60
Db 26 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRRI 85
QY 61 EVPLNERICLVQGSQCSNTESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 120
Db 86 EVPLNERICLVQGSQCSNTESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 145
QY 121 LQGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 180
Db 146 LQGRNTSPDNTYLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSFEGHVSQIMV 205
QY 181 KDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCLFYVEVNN 240
Db 206 KDNAGIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLYQWENPQNFISRCLFYVEVNN 265
QY 241 SQTETHNVFYQBAKCNPFERNVENTSCFMVPGVLPDNLTVIRVKTNKLCEYDDKL 300
Db 266 SQTETHNVFYQBAKCNPFERNVENTSCFMVPGVLPDNLTVIRVKTNKLCEYDDKL 325
QY 301 WSNWSQEMSIGKKRNSTLYI 320
XX
XX
```

The present sequence is that of a protein capable of binding human interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence of IL-4 receptor alpha. It was deduced from cDNA (see A989907) isolated from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1

CC polypeptide can be used to inhibit IL-13 or IL-4 induced IgE synthesis in
 CC B cells, useful in the treatment of diseases in which IgE or Th2
 CC differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
 CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
 CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
 CC them which have been shed from cells as a result of disease, e.g. cancer,
 CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
 CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
 CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
 CC syndrome and toxoplasmosis
 XX
 SQ Sequence 427 AA;

Query Match 100.0%; Score 1760; DB 4; Length 427;
 Best Local Similarity 100.0%; Pred. No. 4.1e-164;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETQPPVNLVSVENLCTVIWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
 DB 27 APTETQPPVNLVSVENLCTVIWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
 QY 61 EPLNERICLVGSCSTNESEKPSILVEKCI SPPEGDPESAVTELQCIWHNLSYMKCSW 120
 DB 87 EPLNERICLVGSCSTNESEKPSILVEKCI SPPEGDPESAVTELQCIWHNLSYMKCSW 146
 QY 121 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
 DB 147 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
 QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFI SCLFYEVEVNN 240
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFI SCLFYEVEVNN 266
 QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300
 DB 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 326
 QY 301 WSNWSQEMSIGKKRNSTLYI 320
 DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 5

ADFL7835
 ID ADFL7835 standard; protein; 427 AA.

XX
 AC ADFL7835;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human IL-13 alpha 1 receptor (IL-13R) protein.
 XX
 KW IL-13R; human; receptor; anaphylaxis; hay fever; asthma;
 KW antiinflammatory; cytostatic; antiulcer; dermatological; antiallergic;
 KW antisthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;
 KW scleroderma; allergic rhinitis; oncological;
 KW chronic obstructive pulmonary disease.

XX Homo sapiens.

XX WO2003080675-A2.

XX 02-OCT-2003.

XX 21-MAR-2003; 2003WO-AU000352.

XX 22-MAR-2002; 2002AU-00001301.

PR 03-FEB-2003; 2003AU-00900437.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Dunlop FM, Baca M, Nash AD, Fabri LJ;

XX
 DR
 DR

WPI; 2003-876912/81.
 N-PSDB; ADFL7834.

XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
 PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
 PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
 PT inflammatory disorder.

XX Disclosure; SEQ ID NO 4; 99pp; English.

XX This invention relates to a novel antibodies that function as interleukin
 CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
 CC for treating certain conditions induced by IL-13. Specifically, it refers
 CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
 CC and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
 CC system, such that it is involved in the induction of IgE, IgG4 and T-
 CC helper cells and accordingly is implicated in conditions from anaphylaxis
 CC to hay fever and asthma. As such, the present invention describes these
 CC novel antibodies as antiinflammatory, cytostatic, antiulcer, and
 CC dermatological, antiallergic and antiasthmatic. The methods, and
 CC compositions are useful for treating various disorders including
 CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
 CC rhinitis, oncological conditions and chronic obstructive pulmonary
 CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
 CC protein of the invention.

XX Sequence 427 AA;

Query Match 100.0%; Score 1760; DB 7; Length 427;
 Best Local Similarity 100.0%; Pred. No. 4.1e-164;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVNLVSVENLCTVIWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60

DB 27 APTETQPPVNLVSVENLCTVIWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86

QY 61 EPLNERICLVGSCSTNESEKPSILVEKCI SPPEGDPESAVTELQCIWHNLSYMKCSW 120

DB 87 EPLNERICLVGSCSTNESEKPSILVEKCI SPPEGDPESAVTELQCIWHNLSYMKCSW 146

QY 121 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180

DB 147 LPGRNTSPDNTYLYWHRSLKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206

QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFI SCLFYEVEVNN 240

DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYQWENPQNFI SCLFYEVEVNN 266

QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 300

DB 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKL CYEDDKL 326

QY 301 WSNWSQEMSIGKKRNSTLYI 320

DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 6

ADFL7812

ID ADFL7812 standard; protein; 427 AA.

XX ADFL7812;

XX 20-MAY-2004 (first entry)

XX Human interleukin-13 receptor alpha (IL-13 Ralpha) protein.

XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;

XX eczema; asthma; AIDS; gene therapy; interleukin; receptor.

XX Homo sapiens.

PH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide
FT Domain 27..427
FT Domain /note= "Human mature IL-13 R protein"
FT Domain 27..347
FT Domain /note = Extracellular domain
FT Domain 327..331
FT Domain /note = WSXWS motif
FT Domain 368..427
FT Domain /note = Cytoplasmic domain
XX US2004043921-A1.
XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX N-PSDB; ADL71811.
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX Claim 1; SEQ ID NO 9; 27pp; English.
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) protein.
XX Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPRGNTSDPTNTLYYHRSLEKIHQENIFREGQYFGCSFDLTTKVKDSSPQHSVQIMV 180
DB 147 LPRGNTSDPTNTLYYHRSLEKIHQENIFREGQYFGCSFDLTTKVKDSSPQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRKVPDPPIKXNLSFHNDLLVQWENPNQFTSRCLFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRKVPDPPIKXNLSFHNDLLVQWENPNQFTSRCLFYEVEVNN 266
QY 241 SQTETHNVPYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
DB 267 SQTETHNVPYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320

DB 327 WSNWSQEMSIGKKRNSTLYI 346
RESULT 7
ADL71814
ID ADL71814 standard; protein; 427 AA.
XX AC ADL71814;
XX 20-MAY-2004 (first entry)
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
XX eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
XX mutein.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 358 /note= "Wild-type Gly is substituted with Asp"
FT FT
XX US2004043921-A1.
XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX Claim 14; Page; 27pp; English.
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
XX specification, however it is constructed based on human IL-13 Ralpha
XX protein shown as SEQ ID NO:9 in the specification.
XX Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EYPLNERICLQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146

QY 121 LPRGNTSPDNTYTLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYTLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISRCLEFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISRCLEFYEVEVNN 266
QY 241 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVIRVKTNKLICYEDDKL 300
Db 267 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVIRVKTNKLICYEDDKL 326
QY 301 WSNWSQEMSIGKRNSTLYI 320
Db 327 WSNWSQEMSIGKRNSTLYI 346
RESULT 8
ADL82843
ID ADL82843 standard; protein; 427 AA.
XX AC ADL82843;
XX DT 17-JUN-2004 (first entry)
XX DE Human PRO2537, SEQ ID 45.
XX KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO: B cell related disorder; cancer;
KW Immune-mediated inflammatory disease; human.
XX OS Homo sapiens.
XX PN WO2004024097-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US029097.
XX PR 16-SEP-2002; 2002US-0411392P.
XX PA (GETH) GENENTECH INC.
XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX WPI: 2004-329389/30.
XX N-PSDB; ADL82842.
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX Claim 10; Fig 45; 695pp; English.
XX The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.

XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETOPPTNLSVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 27 APTETOPPTNLSVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 61 EYPLNERICLOVGSQCSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLSYMKCSW 120
Db 87 EYPLNERICLOVGSQCSTNESEKPSILVEKICISPPGDPESAATELQCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYTLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYTLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISRCLEFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLIVQWENPQNFISRCLEFYEVEVNN 266
QY 241 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVIRVKTNKLICYEDDKL 300
Db 267 SQTETHNVFVQBAKCNPEFRNVENTSCFMVPGVLPDTLNTVIRVKTNKLICYEDDKL 326
QY 301 WSNWSQEMSIGKRNSTLYI 320
Db 327 WSNWSQEMSIGKRNSTLYI 346
RESULT 9
ADN04504
ID ADN04504 standard; protein; 427 AA.
XX AC ADN04504;
XX DT 01-JUL-2004 (first entry)
XX DE Antipsoriatic protein sequence #445.
XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX OS Homo sapiens.
XX PN WO2004028479-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX PR 25-SEP-2002; 2002US-0414006P.
XX PA (GETH) GENENTECH INC.
XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX WPI: 2004-305105/28.
XX N-PSDB; ADN04503.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX Claim 9; SEQ ID NO 898; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

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XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. NO. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLQVGSQCSTNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EVPLNERICLQVGSQCSTNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPGRTSPDNTYLYWHRSLKIHQCEINFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPGRTSPDNTYLYWHRSLKIHQCEINFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCCLFYEVVNN 266
QY 241 SOTETHNVFVVOEAKCENPERNVNTSCPMVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB 267 SOTETHNVFVVOEAKCENPERNVNTSCPMVPGVLPDNTLVIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 10
ID ADN62575 standard; protein; 427 AA.
XX AC ADN62575;
XX 12-AUG-2004 (first entry)
XX Human interleukin 13 (IL-13) receptor alpha 1 chain.
XX Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;
XX IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX cancer; inflammatory disease; rheumatoid arthritis;
XX inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
XX Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
XX Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
XX Lyme disease; tuberculosis; malaria; leishmaniasis.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT 1..26 /note= "Signal peptide"
XX FT Protein 27..427
XX FT /note= "Mature protein claimed in claim 1"
XX US6743604-B1.
XX 01-JUN-2004.
XX 06-APR-2000; 2000US-00545002.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA
XX PI Bonnefoy J, Gauchat J;
XX WPI; 2004-409324/38.

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DR N-PSDB; ADN62574.
XX New isolated nucleic acid molecule encoding a polypeptide capable of
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in
PT diagnostics or for producing antibodies.
XX Claim 1; SEQ ID NO 9; 24pp; English.
XX The invention relates to an isolated nucleic acid molecule (ADN62574),
CC which encodes the mature form of a polypeptide capable of binding human
CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated
CC IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are
CC a vector comprising the nucleic acid molecule and a host cell comprising
CC the vector. The nucleic acids are useful as probes or primers or in the
CC analysis of allelic variation. The polypeptides are useful for binding
CC human IL-13 and/or binding human IL-4 and act as inhibitors by
CC interfering with the interaction between human IL-13 or IL-4 and their
CC natural receptors. They can also be used in medicine, e.g. for treatment
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,
CC Lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be
CC used for producing antibodies, which can be used for diagnosing diseases.
CC The present sequence represents IL-13 receptor alpha 1 subunit.
XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. NO. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLQVGSQCSTNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EVPLNERICLQVGSQCSTNESEKPSILVEKISPEGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPGRTSPDNTYLYWHRSLKIHQCEINFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
DB 147 LPGRTSPDNTYLYWHRSLKIHQCEINFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCCLFYEVVNN 266
QY 241 SOTETHNVFVVOEAKCENPERNVNTSCPMVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB 267 SOTETHNVFVVOEAKCENPERNVNTSCPMVPGVLPDNTLVIRVKTNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 11
ID ABM82441 standard; protein; 427 AA.
XX AC ABM82441;
XX 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX Tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;

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KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.

XX Homo sapiens.

XX WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI: 2004-347921/32.

XX N-PSDB; ACN41073.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 6271; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX Sequence 427 AA;

Query Match 100.0%; Score 1760; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVITWNPPEGASSNCSLWYFSGDKQDKKIAPETRISI 60
DB 27 APTETOPPVTNLVSVENLCTVITWNPPEGASSNCSLWYFSGDKQDKKIAPETRISI 86
QY 61 EVPLNERICLVQGSQSTNESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQGSQSTNESEKPSILVEKICISPPGDPESAVTELCQIWHNLSYMKCSW 146
QY 121 LPCRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 180
DB 147 LPCRNTSPDNTYLYWHRSLKIHQENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 206
QY 181 KDNAGIKPSFNTVPLTSRVKPPPHIKNLSFNDLLYQWENPQNFISRCLPFYEVVNN 240
DB 207 KDNAGIKPSFNTVPLTSRVKPPPHIKNLSFNDLLYQWENPQNFISRCLPFYEVVNN 266
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMWPGVLPDTLNTVIRVKTNKLKYEDDKL 300

Db 267 SQTETHNVFVQBAKCNPEFERNVENTSCFMWPGVLPDTLNTVIRVKTNKLKYEDDKL 326
QY 301 WSNWSQEMSIGKKRNSTLYI 320
DB 327 WSNWSQEMSIGKKRNSTLYI 346
RESULT 12
AAB19808
ID AAB19808 standard; protein; 427 AA.
XX
AC AAB19808;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human interleukin-13 receptor alpha-1 variant.
XX
KW Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FT Peptide 1..26
FT Domain /label= Sig_peptide
FT 27..347
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Misc-difference 130
FT /note= "Gly in "
FT Peptide 327..331
FT /note= "WSXWS motif conserved in the type-I cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 388..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXXQ motif, consensus for STAT binding"

XX US6143871-A.

XX 07-NOV-2000.

XX 12-NOV-1997; 97US-00969125.

XX 13-DEC-1996; 96GB-00025899.

XX (GAUC/) GAUCHAT J.
XX (BONN/) BONNEFOY J.

XX Gauchat J, Bonnefoy J;

XX WPI; 2001-006445/01.

XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.

XX Claim 4; -; 26pp; English.

XX The present sequence is that of a claimed isolated polypeptide which is
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-
CC 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a
CC sequence (see AAB19807) deduced from isolated cDNA by having residue 130
CC as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13
CC receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4
CC induced IGE synthesis in B cells, useful in the treatment of diseases in
CC which Ige or Th2 differentiation plays a role, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised
CC against the polypeptide are useful for detecting IL-13 and IL-4 receptor

PN WO200177171-A2.
XX 18-OCT-2001.
PD 03-APR-2001; 2001WO-US010872.
XX 05-APR-2000; 2000US-0194731P.
PR 28-JUL-2000; 2000US-0222121P.
XX (ZYMO) ZYMOGENETICS INC.
PA Sprechter CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
PI WPI; 2002-025898/03.
XX N-PSDB; AAD22979.
DR Novel soluble receptor polypeptides and polynucleotides used as cytokine
XX antagonist for stimulating ligand activity-induced proliferation of
PT hematopoietic cells and for suppressing immune response in a mammal.
PT
XX Claim 29; Page 236-237; 243pp; English.
XX The invention relates to an isolated soluble zalphal cytokine receptor
XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC haematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is human soluble cytokine IL-13 receptor alpha (IL-13RA1)
CC protein related to the invention
XX
XX Sequence 322 AA;
Query Match 99.1%; Score 1745; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.2e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFQKDKKIAPIETRRSI 60
Db 6 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFQKDKKIAPIETRRSI 65
Qy 61 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 66 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELCIWHNLSYMKCSW 125
Qy 121 LPRGNTSPDNTNLTYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDSFEGHSVQIMV 180
Db 126 LPRGNTSPDNTNLTYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDSFEGHSVQIMV 185
Qy 181 KDNAGIKPFSNIVPLTSRVKPPPHIKNLSFNDDLYVQWENPQNFISRLCFYEVEVNN 240
Db 186 KDNAGIKPFSNIVPLTSRVKPPPHIKNLSFNDDLYVQWENPQNFISRLCFYEVEVNN 245
Qy 241 SQETHNVFVYQAKCENPFRNVENTSCFMVPGVL PDLTNTVRVTKNKL CYEDDKL 300
Db 246 SQETHNVFVYQAKCENPFRNVENTSCFMVPGVL PDLTNTVRVTKNKL CYEDDKL 305
Qy 301 WSNWSQEMSIGKRNST 317
Db 306 WSNWSQEMSIGKRNST 322
RESULT 15
ADFI7841
ID ADFI7841 standard; protein; 664 AA.
XX

AC ADFI7841;
XX 12-FEB-2004 (first entry)
DT Chimeric human IL-13R alpha 1-gp130 fusion protein.
XX Chimeric human IL-13R alpha 1-gp130 fusion protein.
DE IL-13R alpha 1-gp130; human; receptor; chimeric; anaphylaxis; hay fever;
XX asthma; antiinflammatory; cycostatic; antitumor; dermatological;
KW antiasthmatic; fibrosis; Hodgkin's disease;
KW ulcerative colitis; scleroderma; allergic rhinitis; oncological;
KW chronic obstructive pulmonary disease.
XX Chimeric.
OS Homo sapiens.
XX WO2003080675-A2.
PN 02-OCT-2003.
XX 21-MAR-2003; 2003WO-AU000352.
XX 22-MAR-2002; 2002AU-00001301.
PR 03-FEB-2003; 2003AU-00900437.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Dunlop FM, Baca M, Nash AD, Fabri LJ;
PI WPI; 2003-876912/81.
XX N-PSDB; ADFI7840.
DR New monoclonal antibodies against interleukin-13 receptor alpha, useful
XX for treating fibrosis, Hodgkin's disease, ulcerative colitis,
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
PT inflammatory disorder.
XX Disclosure; SEQ ID NO 10; 99pp; English.
XX This invention relates to a novel antibodies that function as interleukin
CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
CC for treating certain conditions induced by IL-13. Specifically, it refers
CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
CC and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
CC system, such that it is involved in the induction of IgE, IgG4 and T-
CC helper cells and accordingly is implicated in conditions from anaphylaxis
CC to hay fever and asthma. As such, the present invention describes these
CC novel antibodies as antiinflammatory, cycostatic, antitumor,
CC dermatological, antiasthmatic and antiasthmatic. The methods and
CC compositions are useful for treating various disorders including
CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
CC rhinitis, oncological conditions and chronic obstructive pulmonary
CC disease. This polypeptide sequence is the chimeric human IL-13R alpha 1-
CC gp130 fusion protein of the invention.
XX
XX Sequence 664 AA;
Query Match 99.1%; Score 1745; DB 7; Length 664;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFQKDKKIAPIETRRSI 60
Db 45 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFHFQKDKKIAPIETRRSI 104
Qy 61 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 105 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELCIWHNLSYMKCSW 164
Qy 121 LPRGNTSPDNTNLTYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDSFEGHSVQIMV 180
Db 165 LPRGNTSPDNTNLTYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDSFEGHSVQIMV 224
Qy 181 KDNAGIKPFSNIVPLTSRVKPPPHIKNLSFNDDLYVQWENPQNFISRLCFYEVEVNN 240

Db 225 KDNAGKIKPSFNIVPLTSRVKPDPPHIXNLSFHNDLLVQWENPQNFISRCLFYEVVNN 284
Qy 241 SQTETHNVFYVOEAKCENPEPERNVENTS CFMVPGLPDTLNTVRI RVKTNKLCYEDDKL 300
Db 285 SQTETHNVFYVOEAKCENPEPERNVENTS CFMVPGLPDTLNTVRI RVKTNKLCYEDDKL 344
Qy 301 WSNWSQEMSICKKRNST 317
Db 345 WSNWSQEMSICKKRNST 361

Search completed: February 8, 2006, 21:59:10
Job time : 99.483 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 18.9712 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APETQPPVNLVSVENLCTIWTNPPPEGASNCSLWYFSHFQDKQDKKIAPETRRSIEV 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.5	72.4	426	2 JC7773	IL-13ralpha 1 prot
2	281	16.0	415	2 S12357	interleukin-5 rece
3	229	13.0	335	2 A40267	interleukin-5 rece
4	228	13.0	420	2 S21052	interleukin-5 rece
5	192	10.9	348	2 JC7907	common cytokine re
6	186.5	10.6	373	2 A55718	interleukin-2 rece
7	181.5	10.3	369	2 A42565	interleukin-2 rece
8	170	9.7	831	2 JQ1655	prolactin receptor
9	168.5	9.6	918	2 A36337	membrane glycoprot
10	162.5	9.2	333	2 S13684	granulocyte-macrop
11	162.5	9.2	400	2 S06945	granulocyte-macrop
12	162	9.2	369	2 I49280	interleukin-2 rece
13	156.5	8.9	378	2 S50040	granulocyte-macrop
14	147.5	8.4	581	2 I45971	prolactin receptor
15	147.5	8.4	616	2 A30304	prolactin receptor
16	147	8.4	1092	2 JX0312	differentiation-at
17	146	8.3	897	1 A3255	cytokine receptor
18	145.5	8.3	830	2 I50455	prolactin receptor
19	145	8.2	396	2 S22909	interleukin-3 rece
20	145	8.2	630	2 I51086	prolactin receptor
21	144	8.2	918	2 A44257	interleukin-6 sign
22	142.5	8.1	896	2 I56563	interleukin-3 rece
23	142.5	8.1	917	2 I49699	glycoprotein 130 -
24	138.5	7.9	310	2 A29884	prolactin receptor
25	138.5	7.9	412	2 A41070	prolactin receptor
26	138.5	7.9	610	2 A34631	lactogen receptor
27	138.5	7.9	610	2 A36116	prolactin receptor
28	138	7.8	896	1 A35782	cytokine receptor
29	138	7.8	1097	2 S17308	leukemia inhibitor

30	136	7.7	878	1 A40091	interleukin-3 rece
31	135.5	7.7	286	2 S50039	granulocyte-macrop
32	130.5	7.4	292	2 I77525	prolactin receptor
33	130.5	7.4	303	2 I77524	prolactin receptor
34	130.5	7.4	608	2 I53269	prolactin receptor
35	130	7.4	289	2 B59405	prolactin receptor
36	130	7.4	376	2 A59405	prolactin receptor
37	130	7.4	622	2 A40144	prolactin receptor
38	123	7.0	378	2 A40266	interleukin-3 rece
39	117	6.6	1471	2 T19506	hypothetical prote
40	116.5	6.6	2029	1 TDFELK	protein-tyrosine-p
41	110.5	6.3	825	1 A60386	interleukin-4 rece
42	108.5	6.2	1268	1 A39640	neural cell adhesi
43	108	6.1	13055	2 T16580	hypothetical prote
44	107	6.1	557	2 A32694	interferon alpha/b
45	106.5	6.1	1259	2 A43425	Bravo/Nr-CAM Cell

ALIGNMENTS

RESULT 1

JC7773

IL-13ralpha 1 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: JC7773

R:Pierrrot, C.; Beniguel, L.; Begue, A.; Khalife, J.

Biochem. Biophys. Res. Commun. 287, 969-976, 2001

A:Title: Expression of a functional IL-13ralpha by rat B cells.

A:Reference number: JC7773; PMID:11573960

A:Accession: JC7773

A:Molecule type: mRNA

A:Residues: 1-426 <PIE>

A:Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251

C:Comment: This protein is an functionally binding protein involved in B cell proliferat

C:Genetics:

A:Gene: il-13ralpha

Query Match 72.4%; Score 1273.5; DB 2; Length 426;
Best Local Similarity 72.4%; Pred. No. 1.4e-94;
Matches 231; Conservative 39; Mismatches 46; Indels 3; Gaps 2;

Qy	3	TETQPPVNLVSVENLCTIWTNPPPEGASNCSLWYFSHFQDKQDKKIAPETRRSIEV	62
Db	27	TEVQPPVNLVSVENLCTIWTNPPPEGASNCSLRYSFHFDDQDKKIAPETRRKKEL	86
Qy	63	PLNERICLVGSGCSTNESEKPSILVEKCIISPPGDPESAATELOCIWHNLSYMKCSWLP	122
Db	87	PLNEKICLVGSGCSTNESEKPSPLVKCISPPRRGSESAVTELOCTWHNLSYMKCSWLP	146
Qy	123	GRNTSPDNTYLYYWHRSLEKIHQCENTFREGQYFGCSFDLTWKVDSFQHSVOIMVKD	182
Db	147	GRNTSPDNTYLYYSSLSGKSLQCENTHREGQHTGSCFKLTKV-ESNYEHNNIQIMVKD	205
Qy	183	NAGTKPSFNVLPTSRVKPPPHIKNLSEHNDLLYQWENPQNFISRCLFYEVENVNSQ	242
Db	206	NAGKIRPSYKLVSTSNVVKPPPHIKHLFLKNGALFVQWKNPQNFSSRCLSYEVENVNSQ	265
Qy	243	TETH--NVFYVQEAACENPEFERNVENTSCFMPVGLPDTLNTVIRVTKNLCYEDDKL	300
Db	266	TDSYNSNSLVEEDKQCNSEFDRNNEGASCFISPGVLXNTVTVTVRVKTNKLCFDDNDL	325
Qy	301	WSNWQEMSIGKRNSTLY 319	
Db	326	WSNWSEALSIGKEPNTFY 344	

RESULT 2

S12357

interleukin-5 receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

Qy 7 PPVTNLVSVENLCTVIWNP-PGASSNCSLWYFSGDKQDKIAPETRRSIEVPLN 65
Db 32 PPV-NFTIKVTGLAQVLLQWPNPDQORNVNLEY-----QVKINAPK-EDDYETRIT 82
Qy 66 ERICLQV-----GSCQSTNESEKPSILVEKICIS-----PPEGDPESAVTELOCIWHNL--- 113
Db 83 ESKCVTILHKGFSASVRTILQNDHSLASSWASAEHLAPGSPGTSVNVLTCTTNTEDN 142
Qy 114 -----SY-----MKCSWLPGRNTSPDTNTYLYWHRSLKIHOCENIFRE--GOYFGCSFDL 163
Db 143 YSRLRSYQVSLHCTWLVGTAPEDTQYPLYRYGSWTE--ECQYSKDTLGRNIACWPPR 200
Qy 164 TKVKDSSPEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVOWEN 223
Db 201 TFIILSKGDMJLAVIYVSSGSKSHALRPFDQLFALHAIDQINPLNVATBIEGTRLSIQWEK 260
Qy 224 PON-FISRCIFYEVEVNNSTQETHNVFYVQBAKCNPEFERNVENTSCFMVPGVLPDTLN 282
Db 261 PVSAPPFHCYDYEKVIHNRNG-----VLQIEKLMTNAFISIIDLSKY----- 304
Qy 283 TVRIRVTKNLCYEDDDKLMNSWQMSIGKKNSTL 318
Db 305 DVQVRAAVSMCREAG-LWSEWSQPIYVGNDEHKPL 339
RESULT 5
JC7907
common cytokine receptor gamma chain, isoform a - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C:Accession: JC7907
R:Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:Title: Identification of an alternatively spliced isoform of the common cytokine receptor gamma chain, expressed as a transmembrane glycoprotein, is a novel member of the gamma chain family.
A:Reference number: JC7907; MUID:22325486; PMID:12437989
A:Accession: JC7907
A:Molecule type: mRNA
A:Residues: 1-348 <MIN>
A:Cross-references: UNIPROT:Q8AUP2; UNIPARC:UPI00000FE604; GB:AJ419897; GB:AJ419898
A:Experimental source: egg
C:Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of the gamma chain family.
C:Genetics:
A:Gene: ch gamma-c-a
Query Match 10.9%; Score 192; DB 2; Length 348;
Best Local Similarity 27.7%; Pred. No. 7e-08;
Matches 64; Conservative 39; Mismatches 88; Indels 40; Gaps 13;
Qy 93 SP-PEGDPESAVTELOCIWHNL-SYMKCSWLPGRNTSPDTNTYLYWHRSLKIHOCEN-I 150
Db 23 SPSPKG-----VECILFNEBYMTCTWGSQTLT--ANYSLYYWYENKLPVVECCOYL 72
Qy 151 FREGQYFGCSFDLTCKVSDSSPEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPDPPHINKL 210
Db 73 WDRSVRIGCFRQSEI--IQFOAFYVRVNASCGTLEIPSNRMSLQNLVKEAP--VNL 128
Qy 211 SFHN-----DDLYVOWENPQNFISRCIFYEVEV--NNSQTETHNVFYVQBAKCNPEFERNVE 266
Db 129 TIHNSGNGQLQUTWSGPP-KEQCLHEVVKYSKDTSWN-----QEVK----- 172
Qy 267 NTSCEFVPGVLPDTLNTVIRVTKNLCYEDDDKLMNSWQMSIGKKNST 317
Db 173 -GVIFSPFSVDYKYYTFVVRSKINNYC-GNTQLMSEWSVPVFWG--NNST 219
RESULT 6
A55718
interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55718

R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, P.
Genomics 23, 69-74, 1994
A:Title: IL-28gamma gene microdeletion demonstrates that canine X-linked severe combined immunodeficiency is caused by a deletion of the IL-28gamma gene.
A:Reference number: A55718; MUID:95130114; PMID:7829104
A:Accession: A55718
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <HEN>
A:Cross-references: UNIPROT:P40321; UNIPARC:UPI0000128CA1; GB:U04361; NID:9517411; PIDN:
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication
Query Match 10.6%; Score 186.5; DB 2; Length 373;
Best Local Similarity 25.4%; Pred. No. 2.1e-07;
Matches 65; Conservative 41; Mismatches 115; Indels 35; Gaps 11;
Qy 62 VPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNL-SYMKCSW 121
Db 21 VGLNSTVPMPNG-----NEDITPDFLTATSEVSSLPPEVQCFFVVEYNNCTWN 75
Qy 122 PGRNTSPDTNTYLYWHRSL--EKIHOCEN-IFREGQYFGCSFDLTCKVSDSSPEQHSQV 178
Db 76 SSSEPRP-TNLTLYWYKNSNDKQVCGHYLFSREVTAGCW--LQKEEIHLYETFFVQL 132
Qy 179 MVKDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN-----DDLYVOWENPQNFISRCIFYE 235
Db 133 --RDPREPRQSTQKQLQNLVLPWAP--ENLTNLHNLSESQLELSWSN--RHLDHCLSHV 186
Qy 236 VEVNSQTETHNVFYVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCY 295
Db 187 VQYRSDWDRSWT-----EQSVDRHSFSLPSVDGQKFTFRVRSRYNPLCG 232
Qy 296 EDDKLMNSWQMSIG 311
Db 233 SAQR-WSEWSHPHWG 247
RESULT 7
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: A42565; A46591; I54332
R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883; PMID:1631559
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: UNIPROT:P31785; UNIPARC:UPI0000000DEA; GB:D11086; NID:G303611; PIDN:
A:Experimental source: MOLT beta lymphoid cells
A>Note: Sequence extracted from NCBI backbone (NCBIP:109167)
R:Nozuchi, M.; Adelstein, J.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887; PMID:8514792
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L12183; NID:G307056; PIDN:AAAS9145.1; PID:
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; H.
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link
A:Reference number: I54332; MUID:94004847; PMID:8401490
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: UNIPARC:UPI0000000DEA; GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:
C:Genetics:

A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross-references: GDB:134807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A;Note: defects are associated with an X-linked form of severe combined immunodeficiency
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 10.3%; Score 181.5; DB 2; Length 369;
Best Local Similarity 26.8%; Pred. No. 5.3e-07;
Matches 61; Conservative 39; Mismatches 87; Indels 41; Gaps 12;

Qy 105 ELQCIWHNLVSKCSWLPGRNTPDNTYLYYHRSLL-EKIHQCN-IFREGQYFCSP 161
Db 59 EVQCFFVNEVMCTWNSSEPQ-TNLTHLYTKNSDNDKVKQCHLYFSEETSGC-- 115
Qy 162 DLTKVKDSSFEQHSQVQWVNDNAGKIKPFSNIVPLTSRVKPDPPHKNLSFPH--NDLTY 218
Db 116 QLQCKEHLVQTFVQL--QDPREPRQATQMLKQLNLVLPWAP--ENLTLKLSQLE 171
Qy 219 VQWENPQNFISRL-----FYEVVNSQTEHNVFYVQEAACENPEFERNVENTSCPMVP 274
Db 172 LNMNN--RFLNHCLEHLVQVYRTWDHSGT-----EQSDVVRHKFSLP 211
Qy 275 GVLPDPLTNTVIRVKTNKLKYEDDKLWSNQEMSIG---KKNSTLY 319
Db 212 SVDGQKRYTFRVRSRPNLC-GSAQHSWSHPIHWGNTSKGNPFLF 258

RESULT 8
JQ1555
Prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:Q222848; PID
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <NAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covalent)

Query Match 9.7%; Score 170; DB 2; Length 831;
Best Local Similarity 23.2%; Pred. No. 1.2e-05;
Matches 79; Conservative 45; Mismatches 137; Indels 80; Gaps 17;

Qy 6 QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFHFQDKQKKIAPETRR 58
Db 126 QPGSPV-NLTLETKRSANIMYLAWSPLADASSN---HLVHY---ELRIKPEKE 176
Qy 59 SIEVPLNERICLVGSCSTNE-----SEKPSILVEKCLSP 95
Db 177 EWET-----ISVGQTQCKINRLNAGRYVQVVRTLDPGSEWSSESRHILIPSGQSP 231
Qy 96 EGDPEAVTELOCIWHNLVSKCSWLPGRNTPDNTYLYYHRSLEKIHQCNIPREGQ 155
Db 232 E-----KPTIKRSPKEFTCWKKQLDGGHPNTNLYLSKEGEQVVECDP-YTAG 285
Qy 156 YFGCSPLTKVQSSFBQHSQVQWVNDNAGKIKPFSNIVPLTSRVKPDPP-----HIKNL 210
Db 286 PNSCYFD--KKHTSFMTIYNTVTRATNEMGNSGSDPHYVDVTYVQDPDPVNTLELKP 343
Qy 211 SFHNDLLVQWENPQNFSR-----CLFYEVVNSQTEHNVFYVQEAACENPEFERNVE 266

Db 344 INRKPYLVLTWSPPLADYRSGLTLEYELRLPPEGEWETIFVGQ-QTYKMFSLN-- 400
Qy 267 NTSCFMVPGVLPDPLTNTVIRVKTNKLKYEDDKLWSNQES 307
Db 401 -----PGKVIQIHCKP-----DHHGWSWSE 425

RESULT 9
A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: UNIPROT:P40189; UNIPARC:UPI0000046B12; GB:M57230; NID:g186353; PID:
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

Query Match 9.6%; Score 168.5; DB 2; Length 918;
Best Local Similarity 25.3%; Pred. No. 1.9e-05;
Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

Qy 6 QPVTNLSVSVENLCTVITWNPPEGASSNCSLWYFHFQ-DKQDKKIAPETRRSIEVPL 64
Db 34 ESPVQLHSNFTAVCLVLEKCMDFHVNANYVKTNHFTPIKEQYTIINRTASSVTFD 93
Qy 65 NERICLVGSCSTNSEKPSILVEKIS--PREGDPESAIVTELOCIWHNLVSKCSWLP 122
Db 94 IASINIQLTCNLTFTGQLEQNVYGITISGLPPE-KPKN---LSCIVNEGKMKRCWDG 148
Qy 123 GRNTSPDNTVLT--YYHRSLEKIHQCNIPREGQYFGCSFDLTKVKDSSFEQHSQVQIMVK 181
Db 149 GRETHLETFTLSEW--ATHKFADCK--AKRTPTSCTVDYSTV---YFVNIEVWVEAE 201
Qy 182 DNAGKI-KPSFNIVPLTSRVKPDPPHKNLSFPHND-----LYVQWENPQNFSRCLFYE 235
Db 202 NALGKVTSDHINFDVP-YKVKPNPPH--NLSVINSELSILKLTWNTNPSIKSVIILKYN 258
Qy 236 VEVNSQTEHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDPLTNTVIRVKTNKLKY 295
Db 259 IQVTKDASTWS-----QIPP-EDTASTRSSFTVDLKPFTYVFRIR-----CM 302
Qy 296 EDD--KLWSNWSQEMS 309
Db 303 KEDGKGYSWDSWEAS 318

RESULT 10
S13684
granulocyte-macrophage colony-stimulating factor receptor - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S13684; A40989
R;Ashworth, A.; Kraft, A.
Nucleic Acids Res. 18, 7178, 1990
A;Title: Cloning of a potentially soluble receptor for human GM-CSF.
A;Reference number: S13684; MUID:91088339; PMID:2148207
A;Accession: S13684
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-333 <ASH>

A;Cross-references: UNIPROT:P15509; UNIPARC:UPI000002AAAL; EMBL:X54935; NID:G31860; PIDN:R;Raines, M.A.; Liu, L.; Qian, S.G.; Joe, V.; Dipersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A;Title: Identification and molecular cloning of a soluble human granulocyte-macrophage
A;Reference number: A40989; MUID:91376112; PMID:1832774
A;Accession: A40989
A;Molecule type: mRNA
A;Residues: 314-333 <RAI>
A;Cross-references: UNIPARC:UPI000017C140; GB:M73832

Query Match 9.2%; Score 162.5; DB 2; Length 333;
Best Local Similarity 20.5%; Pred. No. 1.6e-05;
Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;

Qy 5 TOPPTNLVSVENLCTVIWTPNPEGAS--SNCSLMYFESHFGDKQDKKIAPEPTRRSIEVP 63
Db 29 TVAPASSLNVRFSR-TMNLSDWCQENTTFSKCFL-----TDKKNRVVEPRLSNNECSC 81

Qy 64 LNERICLVGSCSTNSEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKSCWMLPG 123
Db 82 TFRICLHEGVTFEVHNTSQRGQOKLLYPNSGREGTAAQNFSCFIYNADLMNCTWARG 141

Qy 124 RNTSPDNTYLYYHRSLEKIHQENIFRE--GOYFGCSFD-LTKVKDSSPFOHSVQIMVK 181
Db 142 PTAPRDVQVFLYIRNSKRREIRCPYYIQDSGTHVGCHLDNLGLTSRNY-----FLVN 195

Qy 182 DNAGKIKPSF--NIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF--ISRCLF-YEV 236
Db 196 GTSREIGIQFDSLLDTKKIERFPNPNVTRCNTHCLVRWKQPRTYQKLSYLDQFQOL 255

Qy 237 EVN--NSQTEHNVFYVQEAKEPNEFERNVENTSCFMVPGVLPDLTNTVIRVKTNKLK 294
Db 256 DVHRKNTQPTENLLINVGDLNLR-----YNFPSEPRAKHSVKIRAADVRIL 304

Qy 295 YEDDKLWSNWSQEMSIG 311
Db 305 N-----WSSWSEAIIEFG 316

RESULT 11

S06945
granulocyte-macrophage colony-stimulating factor receptor A precursor - human
N;Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S06945; A41286; A44474
R;Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBO J. 8, 3667-3676, 1989
A;Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimul
A;Reference number: S06944; MUID:90059966; PMID:2555171
A;Accession: S06945
A;Molecule type: mRNA
A;Residues: 1-400 <GEA>
A;Cross-references: UNIPROT:P15509; UNIPARC:UPI0000000C45; EMBL:X17648; NID:G32087; PIDN
R;Crosier, K.E.; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Sieff, C.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
A;Title: A functional isoform of the human granulocyte/macrophage colony-stimulating fac
A;Reference number: A41286; MUID:91352066; PMID:1715577
A;Accession: A41286
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 347-400 <CRO>
A;Cross-references: UNIPARC:UPI000017C141
R;Rappold, G.; Willison, T.A.; Henke, A.; Gough, N.M.
Genomics 14, 455-461, 1992
A;Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2
A;Reference number: A44474; MUID:93052350; PMID:1358805
A;Accession: A44474
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'M', 377-400 <RAP>
A;Cross-references: UNIPARC:UPI00000723FC; GB:S48539; NID:G258858; PIDN:AAB23942.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBI:P117980)

C;Genetics:
A;Gene: GDB:CSF2RA; CSF2R
A;Cross-references: GDB:I11877; OMIM:306250; OMIM:425000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
C;Keywords: glycoprotein; growth factor receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status pred
F;322-346/Domain: transmembrane #status predicted <TM>
F;46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #

Query Match 9.2%; Score 162.5; DB 2; Length 400;
Best Local Similarity 20.5%; Pred. No. 2e-05;
Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;

Qy 5 TOPPTNLVSVENLCTVIWTPNPEGAS--SNCSLMYFESHFGDKQDKKIAPEPTRRSIEVP 63
Db 29 TVAPASSLNVRFSR-TMNLSDWCQENTTFSKCFL-----TDKKNRVVEPRLSNNECSC 81

Qy 64 LNERICLVGSCSTNSEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKSCWMLPG 123
Db 82 TFRICLHEGVTFEVHNTSQRGQOKLLYPNSGREGTAAQNFSCFIYNADLMNCTWARG 141

Qy 124 RNTSPDNTYLYYHRSLEKIHQENIFRE--GOYFGCSFD-LTKVKDSSPFOHSVQIMVK 181
Db 142 PTAPRDVQVFLYIRNSKRREIRCPYYIQDSGTHVGCHLDNLGLTSRNY-----FLVN 195

Qy 182 DNAGKIKPSF--NIVPLTSRVKPDPPHINKLSFNDDLYVQWENPQNF--ISRCLF-YEV 236
Db 196 GTSREIGIQFDSLLDTKKIERFPNPNVTRCNTHCLVRWKQPRTYQKLSYLDQFQOL 255

Qy 237 EVN--NSQTEHNVFYVQEAKEPNEFERNVENTSCFMVPGVLPDLTNTVIRVKTNKLK 294
Db 256 DVHRKNTQPTENLLINVGDLNLR-----YNFPSEPRAKHSVKIRAADVRIL 304

Qy 295 YEDDKLWSNWSQEMSIG 311
Db 305 N-----WSSWSEAIIEFG 316

RESULT 12

I49280
interleukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: I49280; A47514; JN0775; JN0775; S37582; I53398
R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
A;Reference number: A47514; MUID:93391374; PMID:8378320
A;Accession: I49280
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-369 <CAO>
A;Cross-references: UNIPROT:P34902; UNIPARC:UPI00000001949; EMBL:U21795; NID:G727349; PID
A;Accession: A47514
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE2>
A;Cross-references: UNIPARC:UPI00000001949; GB:I20048; NID:G404067; PIDN:AAA39286.1; PID:
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
A;Reference number: JN0592; MUID:93277575; PMID:8503926
A;Accession: JN0592
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <KUM>
A;Cross-references: UNIPARC:UPI00000001949; DDBJ:D13565; NID:G303684; PIDN:BAA02760.1; P
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A;Reference number: JN0775; MUID:93366191; PMID:8359699
A;Accession: JN0775

Job time : 19.9712 secs

Db	70	TLIECPD-YKGGPNSCF--SKKHTSIWKVYITVNAINQMGISSSDPLYVHVTVIVE	126
Qy	202	PDPPHKNLSF---HNDD---LVQWENPON-----FISRCIFYEVEVNNST---E	244
Db	127	PEPP--ANLTLELKHPEDKPYLMIKMSPTTMDVKSGWFI---IQYEIRLKEPKATDWE	181
Qy	245	THNVFYQEAKECENPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKLGYEDDDKLMSNW	304
Db	182	THFTLKQTLKIFN-----LYPGQKYLQVR-----CKPDHGYWSEW	218
Qy	305	SQEMSI 310	
Db	219	SPSSI 224	
RESULT 15			
A30304			
prolactin receptor 2 precursor - rabbit			
N;Alternate names: prolactin receptor, mammary gland			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004			
C;Accession: A30304; A60380			
R;Entry: M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989			
A;Title: Identification and sequence analysis of a second form of prolactin receptor by			
A;Reference number: A30304; MUID:89184578; PMID:2928321			
A;Accession: A30304			
A;Molecule type: mRNA			
A;Residues: 1-616 <EDS>			
A;Cross-references: UNIPROT:P14787; UNIPARC:UPI0000132237; GB:J04510; NID:G165669; PIDN:			
R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.			
Int. J. Biochem. 22, 1089-1095, 1990			
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto			
A;Reference number: A60380; MUID:91146782; PMID:2289615			
A;Accession: A60380			
A;Molecule type: protein			
A;Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167			
A;Cross-references: UNIPARC:UPI000017C5D9; UNIPARC:UPI000017C5DA; UNIPARC:UPI000017C5DB;			
A;Note: the amino end of the mature protein was blocked			
C;Keywords: blocked amino end; glycoprotein; transmembrane protein			
P;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-616/Product: prolactin receptor 2 #status predicted <MAT>			
F;36-221/Domain: cytokine receptor homology <CRS>			
F;235-258/Domain: transmembrane #status predicted <TM>			
F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 8.4%; Score 147.5; DB 2; Length 616;			
Best Local Similarity 26.7%; Pred. No. 0.00055;			
Matches 65; Conservative 29; Mismatches 86; Indels 63; Gaps 14;			
Qy	83	KPSILVKEKISPPGDPESAATELQCIWHNLSYMKCSMLPGRNTSPDTNYTLYYWHSLE	142
Db	30	KDFIP--KCRSEK-----BTFTCWWRPGADGGLPTNYLTLY-HKEGE	69
Qy	143	KI-HOCENIFREGQVFGCSFDLTQVNDSSFEQHSVQIMVKONAGKIKPSFNIVPLTSRVK	201
Db	70	TITHECPD-YKGGPNSCF--SKKHTSIWYIITVATNQMGSVSDPRYVDVTVIVE	126
Qy	202	PDPPHKNLSF---HNDD---LVQWENPONFISR---CLFYEVFV---NNSQTEETHN	247
Db	127	PDPP--VNLTLVKHPEDRKPYLWVKWLPDPTLVDRSGWLTLOYEIRLKEPKAAEWETH-	183
Qy	248	VFYVQEAKECENPEPERNVENTSCFMVPGVLPDPTLNTVIRVKTNKLGYEDDDKLMSNW	307
Db	184	-FAGQQTQ-----FKLSLYPGQKYLQVR-----CKPDHGFWSVWSPE	221
Qy	308	MSI 310	
Db	222	SSI 224	

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 111.316 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APETQPVTNLSVSNLC.....WSNWSQEMSGKKNSTLYI 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No! is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1760	100.0	427	1 I13R1_HUMAN	P78552 homo sapien
2	1760	100.0	427	2 Q5JSL4_HUMAN	Q5JSL4 homo sapien
3	1760	100.0	427	2 Q9BBB4_HUMAN	Q9BBB4 homo sapien
4	1747	99.3	426	2 Q59EG2_HUMAN	Q59EG2 homo sapien
5	1692	96.1	409	2 Q7YRV5_MACACA	Q7YRV5 macaca fasc
6	1532	87.0	401	2 Q6U6T1_SHEEP	Q6U6T1 ovis aries
7	1478	84.0	405	2 Q95LFI_CANFA	Q95LFI canis fami
8	1465.5	83.3	423	2 Q863Z6_PIG	Q863Z6 sus scrofa
9	1444	82.0	349	2 Q97597_BOVIN	Q97597 bos taurus
10	1387	78.8	279	2 Q9UDY5_HUMAN	Q9UDY5 homo sapien
11	1314.5	74.7	424	1 I13R1_MOUSE	O09030 mus musculus
12	1308.5	74.3	424	2 O8C1Z3_MOUSE	O8C1Z3 mus musculus
13	1307.5	74.3	426	2 Q561K3_RAT	Q561K3 rattus norv
14	1302.5	74.0	424	2 Q8BNM4_MOUSE	Q8BNM4 mus musculus
15	1274.5	72.4	426	2 Q8VHC2_RAT	Q8VHC2 rattus norv
16	603.5	34.3	252	2 Q8VDP7_MOUSE	Q8VDP7 mus musculus
17	296	16.8	386	1 I13R2_CANFA	Q951F0 canis fami
18	284	16.1	380	1 I13R2_HUMAN	P21183 homo sapien
19	281	16.0	415	1 IL5RA_MOUSE	P21183 homo sapien
20	278	15.8	383	2 Q88786_MOUSE	Q88786 mus musculus
21	267	15.2	385	2 Q6VHK6_RAT	Q6VHK6 rattus norv
22	253	14.4	391	2 Q6UAN8_TETNG	Q6UAN8 tetraodon n
23	239	13.6	393	2 Q5U516_XENLA	Q5U516 xenopus lae
24	235.5	13.4	415	2 Q920K4_CAVPO	Q920K4 cavia porce
25	235	13.4	414	2 Q920B8_RAT	Q920B8 rattus norv
26	234	13.3	414	2 Q99PS3_RAT	Q99PS3 rattus norv
27	233	13.2	404	2 Q90XP8_ONCMY	Q90XP8 oncorhynch
28	230	13.1	420	1 IL5RA_HUMAN	Q01344 homo sapien
29	229	13.0	333	2 Q15469_HUMAN	Q15469 homo sapien
30	228	13.0	420	2 Q14633_HUMAN	Q14633 homo sapien
31	227	12.9	396	2 Q14631_HUMAN	Q14631 homo sapien

RESULT 1

ID	I13R1_HUMAN	STANDARD	PRT	427 AA
AC	P78552; Q95646; Q9656;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213al antigen).			
GN	Name=IL13RA1; Synonyms=IL13R, IL13RA;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Carcinoma;			
RX	MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;			
RA	Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,			
RA	Ferrara P.;			
RT	"Cloning of the human IL-13R alpha chain and reconstitution with the			
RT	IL4R alpha of a functional IL-4/IL-13 receptor complex.";			
RL	FEBS Lett. 401:163-166(1997).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=B-cell;			
RA	Gauchat J.F.M., Schlagenhaut E., Peng N.P., Moser R., Yanage M.,			
RA	Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,			
RA	Eugster H.P., Bonnefoy J.Y.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;			
RA	Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;			
RT	"cDNA cloning and characterization of the human interleukin 13			
RT	receptor alpha chain.";			
RL	J. Biol. Chem. 271:29265-29270(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Wada M., Hisano T., Kuwano M.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Pancreas;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Raha J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Rha Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; Proc Natl Acad Sci U.S.A. 99:16899-16903(2002).

CC -I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling, but cannot replace the function of gamma C in allowing enhanced IL2 binding activity.

CC -I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1, and possibly other components.

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver, skeletal muscle and ovary; lowest levels in brain, lung and kidney. Also found in B-cells, T-cells and endothelial cells.

CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or activation.

CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5 subfamily.

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CC -----

DR ENBL; Y10659; CAA71669.1; -; mRNA.

DR ENBL; Y09328; CAA70508.1; -; mRNA.

DR ENBL; U62858; AAB37127.1; -; mRNA.

DR ENBL; U81379; AAD00510.3; -; mRNA.

DR ENBL; BC009960; AAH09960.1; -; mRNA.

DR Ensembl; ENSG00000131724; Homo sapiens.

DR HGNC; HGNC:5974; IL13RA1.

DR H-InvDB; HIX0017008; -.

DR MIM; 300119; -.

DR GO; GO:0005898; C:interleukin-13 receptor complex; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.

DR InterPro; IPR002996; Cytok_recept_B/G.

DR InterPro; IPR003532; Hemtptnrecept_F2.

DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.

KW Glycoprotein; Receptor; Signal; Transmembrane.

FT SIGNAL 1 21 Potential

FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.

FT TOPO_DOM 22 343 Extracellular (Potential).

FT TRANSMEM 344 367 Potential.

FT TOPO_DOM 368 427 Cytoplasmic (Potential).

FT MOTIF 327 331 WSXWS motif.

FT MOTIF 374 382 Box 1 motif.

FT CARBOHYD 37 37 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 61 61 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 105 105 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 138 138 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 235 235 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 265 265 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 293 293 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 329 329 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 341 341 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 46 95 Potential.

FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.

FT CONFLICT 130 130 T -> I (in Ref. 3).

FT CONFLICT 358 358 G -> D (in Ref. 3).

SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;

Query Match 100.0%; Score 1760; DB 1; Length 427;

Best Local Similarity 100.0%; Pred. No. 6.3e-130; Indels 0; Gaps 0; Matches 320; Conservative 0; Mismatches 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLMYFHSFGDKQDKKIAPETRRSI 60

Db 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLMYFHSFGDKQDKKIAPETRRSI 86

QY 61 EYPLNERICLVGSCQSTNESEKPSILVKEKISPPGDPESAVTELCIWHNLSYMKCSW 120

Db 87 EYPLNERICLVGSCQSTNESEKPSILVKEKISPPGDPESAVTELCIWHNLSYMKCSW 146

QY 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQVFGCSFDLTWKVDSFSEQHSVQIMV 180

Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQVFGCSFDLTWKVDSFSEQHSVQIMV 206

QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFINDLLYQWENPQNPFISRCIFYEVEVNN 240

Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFINDLLYQWENPQNPFISRCIFYEVEVNN 266

QY 241 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPTLTNIVRVKTNKLCYEDDKL 300

Db 267 SQTETHNVFYQBAKCNPEFERNVENTSCFMVPGVLPTLTNIVRVKTNKLCYEDDKL 326

QY 301 WSNWSQEMSIGKKRNSTLYI 320

Db 327 WSNWSQEMSIGKKRNSTLYI 346

RESULT 2

Q5JSL4 HUMAN

ID Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.

AC Q5JSL4;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Interleukin 13 receptor, alpha 1.

GN Name=IL13RA1; ORFNames=RP13-12804.2-001;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Lawlor S.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).

CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).

CC EMBL; AL391280; CAI41410.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR002996; Cytok_recept_B/G.

DR InterPro; IPR003532; Hemtptnrecept_F2.

DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.

KW Receptor; Transmembrane.

SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;

Query Match 100.0%; Score 1760; DB 2; Length 427;

Best Local Similarity 100.0%; Pred. No. 6.3e-130; Indels 0; Gaps 0; Matches 320; Conservative 0; Mismatches 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLMYFHSFGDKQDKKIAPETRRSI 60

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Db 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCQSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146
Qy 121 LPGRNTSPDNTYTLTYWHRSLKIHQECENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 180
Db 147 LPGRNTSPDNTYTLTYWHRSLKIHQECENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326
Qy 301 WSNWSQEMSIGKGRNSTLIYI 320
Db 327 WSNWSQEMSIGKGRNSTLIYI 346

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RESULT 3
Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.
ID Q96BB4 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q96BB4 HUMAN PRELIMINARY; PRT; 426 AA.
DT 10-MAY-2005 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Hellon E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schen J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).

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DR EMBL; BC015768; AAH15768.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; P:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003532; Hematpntnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC64;

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.3e-130;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 60
Db 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCQSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146
Qy 121 LPGRNTSPDNTYTLTYWHRSLKIHQECENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 180
Db 147 LPGRNTSPDNTYTLTYWHRSLKIHQECENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326
Qy 301 WSNWSQEMSIGKGRNSTLIYI 320
Db 327 WSNWSQEMSIGKGRNSTLIYI 346

RESULT 4
Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
DT 10-MAY-2005 (TremBLrel. 30, Created)
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Tokoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB209849; BAD93086.1; -, mRNA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;

Query Match 99.3%; Score 1747; DB 2; Length 426;
Best Local Similarity 99.7%; Pred. No. 6.6e-129;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 60
Db 26 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 85

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QY 61 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 86 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 145
QY 121 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 146 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 205
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 240
Db 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 265
QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 300
Db 266 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 325
QY 301 WSNWSQEMSIGKGRNSTLYI 320
Db 326 WSNWSQEMSIGKGRNSTLYI 345

RESULT 5
Q7YRV5 MACFA
ID Q7YRV5 MACFA PRELIMINARY; PRT; 409 AA.
AC Q7YRV5
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13ral;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RT "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY312267; AAP78901.1; -; mRNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN 9 409 interleukin 13 receptor alpha 1.
FT NON_TER 1
SQ SEQUENCE 409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match 96.1%; Score 1692; DB 2; Length 409;
Best Local Similarity 95.9%; Pred. No. 1.3e-124;
Matches 307; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 APTEOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHGDKQDKKIAPETRRI 60
Db 9 APTEOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHGDKQDKKIAPETRRI 68
QY 61 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 69 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 128
QY 121 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 129 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 188
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 240
Db 189 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 248
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QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 300
Db 249 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 308
QY 301 WSNWSQEMSIGKGRNSTLYI 320
Db 309 WSNWSQEMSIGKGRNSTLYI 328
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RESULT 6

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Q6U6T1 SHEEP
ID Q6U6T1 SHEEP PRELIMINARY; PRT; 401 AA.
AC Q6U6T1
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin 13 receptor alpha 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maccarone P., Drinkwater C.C., Nash A.D.;
RT "Cloning of the sheep interleukin 13 receptor alpha 1 cDNA.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY377582; AAQ83584.1; -; mRNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT CHAIN <1 401 interleukin 13 receptor alpha 1.
FT NON_TER 1
SQ SEQUENCE 401 AA; 45834 MW; 4E7AD6162BD42B25 CRC64;
```

Query Match 87.0%; Score 1532; DB 2; Length 401;
Best Local Similarity 86.2%; Pred. No. 4.8e-112;
Matches 276; Conservative 17; Mismatches 27; Indels 0; Gaps 0;

```
QY 1 APTEOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHGDKQDKKIAPETRRI 60
Db 1 APAESHPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFHFHGDKQDKKIAPETRRI 60
QY 61 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
Db 61 EVPLNERICLVGSGCSTNESEKPSILVEKCI SPPEGDPSAVTELCQIWHNLSYMKCSW 120
QY 121 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 121 LPRGNTSPDNTNLTLYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 240
Db 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQYQWENPQNFI SRCLFYEVEVNN 240
QY 241 SQTEHNVFVQAKCENPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 300
Db 241 SHAETHDIFVYBEAKCQNTFEFERNLEGTTCFMVPGVLPDNLTVIRVKTNKL CYEDDKL 300
QY 301 WSNWSQEMSIGKGRNSTLYI 320
Db 301 WSNWSQEMSIGKGRNSTLYI 320
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RESULT 7

```
Q95LF1 CANFA
ID Q95LF1 CANFA PRELIMINARY; PRT; 405 AA.
AC Q95LF1;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Interleukin 13 receptor alpha chain 1 (fragment).
GN Name=IL13R1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=21287533; PubMed=11389954; DOI=10.1016/S0165-2427(01)00271-9;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha and
RT alpha2) cDNAs and detection of corresponding mRNAs in canine
RT tissues."
RL Vet. Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314532; AAL14886.1; -; mRNA.
DR Ensembl; ENSCAFG00000018359; Canis familiaris.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW NON TER.
FT
SQ
SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5E3F42 CRC64;

Query Match 84.0%; Score 1478; DB 2; Length 405;
Best Local Similarity 83.4%; Pred. No. 8.6e-108;
Matches 267; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFHFQDKDKKIAPETRRSI 60
DB |||||
DB 5 APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFHFQDKDKKIAPETRRSK 64
DB |||||
QY 61 EVPLNERICLVGSGCSTNSESKEPSILVEKICISPEGDPESAVTELOCIMWNLNLSYMKCSW 120
DB |||||
DB 65 EVPLNERICLVGSGCSTNSESKEPSILVEKICISPEGDPESAVTELOCIMWNLNLSYMKCSW 124
DB |||||
QY 121 LPGRTSPDNTYLYYHRSLEKIHQENIFREGQYFCGSDLTWKVDSSFEQHSVQIMV 180
DB |||||
DB 125 LPGRTSPDNTYLYYHRSLEKIHQENIFREGQYFCGSDLTWKVDSSFEQHSVQIMV 184
DB |||||
QY 181 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB |||||
DB 185 KDNARKIPSNIVPLTSRVKPDPPHINKLSFQNGDLVQWKNPQNFYSRCLSYQVEVNN 244
DB |||||
QY 241 SQTETHNVFYVQEAACENPEFERNVENTSCFVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB |||||
DB 245 SQTETHNVFYVQEAACENPEFERNVENTSCFVPGVLPDNTLVIRVKTNKLCEYDDKL 304
DB |||||
QY 301 WSNWSQMSIGKKNSTLYI 320
DB |||||
DB 305 WSNWSQMSIGKKNSTLYI 324
DB |||||

RESULT 8
Q86326_PIG PRELIMINARY; PRT; 423 AA.
AC Q86326;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
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OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarlega D.S., Dawson H., Krangel H., Solano-Aguilar G.,
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
RT 1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and
RT Trichuris suis infections on tissue mRNA levels."
RL Vet. Immunol. Immunopathol. 101:223-234(2004).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- DOMAIN: The WSWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ
SEQUENCE 423 AA; 47984 MW; EA636FE68CA533D9 CRC64;

Query Match 83.3%; Score 1465.5; DB 2; Length 423;
Best Local Similarity 82.5%; Pred. No. 8.8e-107;
Matches 264; Conservative 23; Mismatches 32; Indels 1; Gaps 1;

QY 1 APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFHFQDKDKKIAPETRRSI 60
DB |||||
DB 24 APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFHFQDKDKKIAPETRHSE 83
DB |||||
QY 61 EVPLNERICLVGSGCSTNSESKEPSILVEKICISPEGDPESAVTELOCIMWNLNLSYMKCSW 120
DB |||||
DB 84 EVPLNERICLVGSGCSTNSESKEPSILVEKICISPEGDPESAVTELOCIMWNLNLSYMKCSW 143
DB |||||
QY 121 LPGRTSPDNTYLYYHRSLEKIHQENIFREGQYFCGSDLTWKVDSSFEQHSVQIMV 180
DB |||||
DB 144 LPGRTSPDNTYLYYHRSLEKIHQENIFREGQYFCGSDLTWKVDSSFEQHSVQIMV 202
DB |||||
QY 181 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB |||||
DB 203 KDNAGKIPSNIVPLTSRVKPDPPHINKLSFQNGDLVQWKNPQNFYSRCLSYQVEVNN 262
DB |||||
QY 241 SQTETHNVFYVQEAACENPEFERNVENTSCFVPGVLPDNTLVIRVKTNKLCEYDDKL 300
DB |||||
DB 263 TQAKTHDIFYVEEAKQNSPEEGNLEGMICFVPGVLPDNTLVIRVKTNKLCEYDDKL 322
DB |||||
QY 301 WSNWSQMSIGKKNSTLYI 320
DB |||||
DB 323 WSNWSQMSIGKKNSTLYI 342
DB |||||

RESULT 9
Q97597_BOVIN PRELIMINARY; PRT; 349 AA.
AC Q97597;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20080132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
RA Trigona W.L., Brown W.C., Estes D.M.;
```

RT "Functional implications for signaling via the IL4R/IL13R complex on
RT bovine cells";
RL Vet. Immunol. Immunopathol. 72:73-79(1999).
DR EMBL; AF074402; AAC98147.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
KW Receptor.
FT NON_TER 1
FT TER 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 82.0%; Score 1444; DB 2; Length 349;
Best Local Similarity 84.0%; Pred. No. 3.4e-105;
Matches 262; Conservative 15; Mismatches 35; Indels 0; Gaps 0;

QY 9 VTNLSVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETRRI 68
DB 1 VTNLSVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETRRI 60

QY 69 CLQVGSQCSNTESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKSWLPGRNTSP 128
DB 61 CLQVGSQCSNTESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKSWLPGRNASP 120

QY 129 DTYNTLYWHRSLLEKIHQCNIFREGQYFGCSFDLTVKVDSSFEQHSVQIMVKDNAGKIK 188
DB 121 DPNVILYWHNSLGLKIQCNIFREGQYFGCSFDLTVKVDSSFEQHSVQIMVKDNAGKIS 180

QY 189 PSFNIVPLTSRVKDPDPHINKLSFNHDDLVOVENPQNFISRCIFYEVEVNNQSTETHNV 248
DB 181 PSFNIVPLTSRVKDPDPHINKLSFNHDDLVOVENPQNFISRCIFYEVEVNNQSTETHNV 240

QY 249 FYVQEAACENPERNVENTSCFWPGVLPDLTNTVIRVTKNKLVCYEDDKLWSNWSQEM 308
DB 241 FYVQEAACQNTPEGNLEGTCIFWPGVLPDLTNTVIRVTKNKLVCYEDDKLWSNWSQAM 300

QY 309 SIGKKNSTLYI 320
DB 301 SIGKANQTFYI 312

RESULT 10
Q9UDY5 HUMAN
ID Q9UDY5 HUMAN PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interleukin-13 receptor soluble form (interleukin 13 receptor, alpha 1).
DE Names=IL13RAL; ORFNames=RPI3-12804.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).

DR EMBL; U81380; AAD00511.2; -; mRNA.
DR EMBL; AL391280; CA141409.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn recept B/G.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;

Query Match 78.8%; Score 1387; DB 2; Length 279;
Best Local Similarity 99.6%; Pred. No. 7.6e-101;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETRRI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSGDKQDKKIAPETRRI 86

QY 61 EYPLNERICLVQSGQCSNTESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSW 120
DB 87 EYPLNERICLVQSGQCSNTESEKPSILVEKICSPPEGDPESAVTELOCIWHNLSYMKCSW 146

QY 121 LPRGNTSPDNTYLYWHRSLLEKIHQCNIFREGQYFGCSFDLTVKVDSSFEQHSVQIMV 180
DB 147 LPRGNTSPDNTYLYWHRSLLEKIHQCNIFREGQYFGCSFDLTVKVDSSFEQHSVQIMV 206

QY 181 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLVOVENPQNFISRCIFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLVOVENPQNFISRCIFYEVEVNN 266

QY 241 SQTETHNVFYVQ 252
DB 267 SQTETHNVFYVR 278

RESULT 11
IL13RI_MOUSE
ID IL13RI_MOUSE STANDARD; PRT; 424 AA.
AC Q09030; Q7TTT27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (interleukin-13 binding protein) (NR4).
DE Names=IL13ral; Synonyms=il13r, il13ra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A., Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."
RN Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Hopskins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity (By similarity).
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13R1,
CC and possibly other components (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
CC testis, stomach, brain, skin, and colon; but not skeletal muscle.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: S80963; AB50695.1; -; mRNA.
DR EMBL: BC052425; AAHS2425.2; -; mRNA.
DR EMBL: BC059939; AAHS9939.1; -; mRNA.
DR Ensembl: ENSMUSG0000017057; Mus musculus.
DR MGI: MGI:105052; IL13ral.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR002996; Cytokn_recept_B/G.
DR InterPro: IPR003532; Hemtpcnrecept_F2.
DR PROSITE: PS01356; HEMATOPO REC S_F2; 1.
KW Glycoprotein; Receptor; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.
FT TOPO_DOM 26 340 Extracellular (Potential).
FT TRANSMEM 341 364 Potential.
FT TOPO_DOM 365 424 Cytoplasmic (Potential).
FT MOTIF 324 328 WSXWS motif.
FT MOTIF 371 379 Box 1 motif.
FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 338 338 N-linked (GlcNAc...) (Potential).
FT DISULFID 44 93 Potential.
FT DISULFID 132 142 By similarity.
FT DISULFID 171 183 By similarity.
SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;
Query Match 74.7%; Score 1314.5; DB 1; Length 424;
Best Local Similarity 74.6%; Pred. No. 6.5e-95;
Matches 238; Conservative 35; Mismatches 45; Indels 1; Gaps 1;
QY 1 APTETQPPVNLVSVENLCTVIWTNPPPEGASSCSLWYFSHFQDKQKIAPIETRISI 60
Db |||||
25 AATEVQPPVNLVSVENLCTVIWTNPPPEGASPNCTLRYSFHFQDKQKIAPIETRKE 84
QY |||||
61 EYPLNERICLQVGSQCSTNESEKPSILVEKICSPPEGDPESAVTELQCIWNLSYMKCSW 120

Db |||||
85 ELPLDEKICLQVGSQCSTNESEKPSILVKKICSPPEGDPESAVTELKCIWNLSYMKCSW 144
QY |||||
121 LRGENTSPDNTYLYTHRSLEKIHOCENIFREGQVFGCSFDLTQKVDSSFEQHSQVIMV 180
Db |||||
145 LPRNTSPDTHYLYTWISLEKSRQCENIYREGQHSFSLTKV-EPSEFQHQVIMV 203
QY |||||
181 KDNAGIKPSFNIVPLTSRVKPPPHIKNLSPFNDDLYQWENPQNPISCLFYEVENVN 240
Db |||||
204 KDNAGIRPSCKIVSLTSYVKPPPHIKLLKNGALLVQWKQNPQNPFRSRCLTYEVENVN 263
QY |||||
241 SQTETNVFVQAEKCNPEFERNVENTSCFMVPGVLPTLNTVTRVTKNLCYEDDKL 300
Db |||||
264 TQTDREHILEVEDKQNSSEDRNMEGTSCFQLPGVLADAVYTRVRVTKNLCFDDNKL 323
QY |||||
301 WSNWSQEMSGKGRNSTLY 319
Db |||||
324 WSDWSEAQSIGKEONSTFY 342
RESULT 12
Q8C1Z3_MOUSE
ID Q8C1Z3_MOUSE PRELIMINARY; PRT; 424 AA.
AC Q8C1Z3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus embryo RCB-0549 Cle-H3 CDNA, RIKEN full-length enriched
DE library, clone:G430044106 product:Interleukin 13 receptor, alpha 1,
DE full insert sequence.
GN Name=Il13ral;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of


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Db 25 AATEVQPPVTNLSVSVENLCTIVTWSPPEGASPNCSLRYFSHFDDQQDKKIAPETRKKEL 84
Qy 61 EVPLNERICLVQGSQCSTNSESKEPSILVEKICISPPGDPDESATVTELOCIWHNLSYMKCSW 120
Db 87 PLNEKICLVQGSQCSTNSESKEPSILVEKICISPPRGRSESATVTELOCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDTNLTLYYHRSLEKIHQENIPREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 182
Db 147 GKNTSPDTNLTLYYHRSLEKIHQENIPREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 205
Qy 183 NAGKIKPSENFIVPLTSRVKPPDPHIIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQ 242
Db 206 NACKIRPSYKIVGFTSNVKEGPHIKHLFLKNGALFVQWKNPQNFSSRCILSYEVEVNSTQ 265
Qy 243 TETH--NVFVQEAKECNPEFERNVENTSCFMVPGVLPDPLTNTVTRVTKNKLCEYEDDKL 300
Db 266 TDSYNSNSLEVEDKQNSFDRNMEGASCIFSPGLANTVYTVRVVQTNKLCFDDNDL 325
Qy 301 WSNWSQEMSGKKRNSTLY 319
Db 324 WSDWSEAQSIGKEPNSTFY 342
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RESULT 15

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Q8VHC2_RAT
ID Q8VHC2_RAT PRELIMINARY; PRT; 426 AA.
AC Q8VHC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-13 receptor alpha 1.
GN Name=Il13ral;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fisher F344;
RC MEDLINE=21458304; PubMed=11573960; DOI=10.1006/bbrc.2001.5682;
RA Pierrot C., Beniguel L., Begue A., Khalife J.;
RT "Expression of a functional IL-13Ralpha1 by rat B cells.";
RL Biochem. Biophys. Res. Commun. 287:969-976(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC EMBL; AY044251; AAK94870.1; -; mRNA.
DR PIR; JC7773; JC7773.
DR Ensembl; ENSRNOG0000013170; Rattus norvegicus.
DR RGD; 628741; Il13ral.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtptnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 426 AA; 48510 MW; 08BPE0E31D9D3C47 CRC64;
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Query Match 72.4%; Score 1274.5; DB 2; Length 426;
Best Local Similarity 72.4%; Pred. No. 9.1e-92;
Matches 231; Conservative 39; Mismatches 46; Indels 3; Gaps 2;
Qy 3 TETQPPVTNLSVSVENLCTIVTWNPPEGASPNCSLRYFSHFDDQQDKKIAPETRKSIEV 62
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Db 27 TEVQPPVTNLSVSVENLCTIVTWNPPEGASPNCSLRYFSHFDDQQDKKIAPETRKKEL 86
Qy 63 PLNERICLVQGSQCSTNSESKEPSILVEKICISPPGDPDESATVTELOCIWHNLSYMKCSWLP 122
Db 87 PLNEKICLVQGSQCSTNSESKEPSILVEKICISPPRGRSESATVTELOCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDTNLTLYYHRSLEKIHQENIPREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 182
Db 147 GKNTSPDTNLTLYYHRSLEKIHQENIPREGQYFGCSFDLTVKYDSSPEOHSVQIMVKD 205
Qy 183 NAGKIKPSENFIVPLTSRVKPPDPHIIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNSQ 242
Db 206 NACKIRPSYKIVGFTSNVKEGPHIKHLFLKNGALFVQWKNPQNFSSRCILSYEVEVNSTQ 265
Qy 243 TETH--NVFVQEAKECNPEFERNVENTSCFMVPGVLPDPLTNTVTRVTKNKLCEYEDDKL 300
Db 266 TDSYNSNSLEVEDKQNSFDRNMEGASCIFSPGLANTVYTVRVVQTNKLCFDDNDL 325
Qy 301 WSNWSQEMSGKKRNSTLY 319
Db 326 WSNWSEALSIGKEPNSTFY 344

Search completed: February 8, 2006, 22:05:55
Job time : 112.316 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:06:20 ; Search time 26.5039 Seconds
(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APTETQPPVTNLSVSVENL.....WSNWSQEMSGKKRNSFLYI 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1760	100.0	426	2	US-09-688-286D-4
2	1760	100.0	427	2	US-08-969-125-9
3	1760	100.0	427	2	US-09-545-002-9
4	1760	100.0	427	2	US-09-943-016-6094
5	1745	99.1	322	2	US-09-825-561A-82
6	1745	99.1	784	2	US-09-313-942-30
7	1745	99.1	784	2	US-10-282-162-30
8	1745	99.1	793	2	US-09-313-942-32
9	1745	99.1	793	2	US-10-282-162-32
10	1478	84.0	405	2	US-09-828-995B-50
11	1314.5	74.7	424	2	US-09-688-286D-2
12	1265	71.9	233	2	US-09-949-016-8550
13	296	16.8	318	2	US-09-828-995B-69
14	296	16.8	365	2	US-09-828-995B-66
15	296	16.8	386	2	US-09-828-995B-61
16	296	16.8	561	2	US-09-828-995B-72
17	296	16.8	561	2	US-09-828-995B-81
18	296	16.8	563	2	US-09-828-995B-78
19	296	16.8	565	2	US-09-828-995B-75
20	284	16.1	317	2	US-09-825-561A-84
21	284	16.1	380	1	US-08-609-572-4
22	284	16.1	380	2	US-08-841-751-4
23	284	16.1	380	2	US-08-846-340-4
24	284	16.1	380	2	US-08-846-344-4
25	284	16.1	380	2	US-09-301-808-4
26	281	16.0	398	1	US-07-757-390-6
27	281	16.0	398	1	US-08-442-282-6

28	281	16.0	398	1	US-08-442-281-6	Sequence 6, Appli
29	281	16.0	398	1	US-08-939-727-6	Sequence 6, Appli
30	281	16.0	415	1	US-07-757-390-5	Sequence 5, Appli
31	281	16.0	415	1	US-08-442-282-5	Sequence 5, Appli
32	281	16.0	415	1	US-08-442-281-5	Sequence 5, Appli
33	281	16.0	415	1	US-08-939-727-5	Sequence 5, Appli
34	281	16.0	415	2	US-09-886-319A-23	Sequence 23, Appli
35	278	15.8	383	1	US-08-609-572-2	Sequence 2, Appli
36	278	15.8	383	2	US-08-841-751-2	Sequence 2, Appli
37	278	15.8	383	2	US-08-846-340-2	Sequence 2, Appli
38	278	15.8	383	2	US-08-846-344-2	Sequence 2, Appli
39	277	15.7	335	2	US-09-301-808-2	Sequence 2, Appli
40	277	15.7	335	1	US-07-947-130-3	Sequence 3, Appli
41	277	15.7	335	1	US-08-421-822-3	Sequence 3, Appli
42	277	15.7	335	1	US-08-421-823-3	Sequence 3, Appli
43	272	15.5	255	2	US-09-828-995B-58	Sequence 58, Appli
44	260	14.8	315	1	US-07-757-390-8	Sequence 8, Appli
45	260	14.8	315	1	US-08-442-282-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

Query Match 100.0%; Score 1760; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APTETQPPVTNLSVSVENLCTVIWTNPPEGASSNCSLWYFSHFQDKQDKKIAPETRSI	60
Db	26	APTETQPPVTNLSVSVENLCTVIWTNPPEGASSNCSLWYFSHFQDKQDKKIAPETRSI	85
Qy	61	EVPLNERICLVGQSCSTNESEKPSILVEKICISPEGDPESAVTELCIWNLSYMKCSW	120
Db	86	EVPLNERICLVGQSCSTNESEKPSILVEKICISPEGDPESAVTELCIWNLSYMKCSW	145
Qy	121	LPGRNTSPDNTYLYWHSLEKHQCNIFREGQYFCSDPDLTKVKDSSFEQHSVQIMV	180
Db	146	LPGRNTSPDNTYLYWHSLEKHQCNIFREGQYFCSDPDLTKVKDSSFEQHSVQIMV	205
Qy	181	KONAGKIPSNIVPLTSRVKPDPPHINKLNFHNDLVQVWENPNQFISRCILFYEVVNN	240
Db	206	KONAGKIPSNIVPLTSRVKPDPPHINKLNFHNDLVQVWENPNQFISRCILFYEVVNN	265
Qy	241	SQTEHNVFYVQEAECENPEFERNVENTSCFMPGVLEDTLNTVIRVKTNKLCEYDDKL	300

Db 266 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 325

Qy 301 WSNWSQEMSGKKRNSTLYI 320
|||||

Db 326 WSNWSQEMSGKKRNSTLYI 345
|||||

RESULT 2

US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTEQPPTNLVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 60
|||||

Db 27 APTEQPPTNLVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 86
|||||

Qy 61 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESA VTELCIWHNLSYMKCSW 120
|||||

Db 87 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESA VTELCIWHNLSYMKCSW 146
|||||

Qy 121 LPRGNTSPDNTLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDS SFEQHSVQIMV 180
|||||

Db 147 LPRGNTSPDNTLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDS SFEQHSVQIMV 206
|||||

Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLFYEVVNN 240
|||||

Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLFYEVVNN 266
|||||

Qy 241 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 300
|||||

Db 267 SQTEHNVFVQEA KCENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKL CYEDDKL 326

Qy 301 WSNWSQEMSGKKRNSTLYI 320
|||||

Db 327 WSNWSQEMSGKKRNSTLYI 346
|||||

RESULT 3

US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTEQPPTNLVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 60
|||||

Db 27 APTEQPPTNLVSVENLCTVIWTWNPPEGASNCSLWYFHFHFGDKQDKKIAPETRRI 86
|||||

Qy 61 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESA VTELCIWHNLSYMKCSW 120
|||||

Db 87 EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESA VTELCIWHNLSYMKCSW 146
|||||

Qy 121 LPRGNTSPDNTLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDS SFEQHSVQIMV 180
|||||

Db 147 LPRGNTSPDNTLYYWHRSLEKIHQCE NIFREGQYFGCSFDLT KVKDS SFEQHSVQIMV 206
|||||

Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLFYEVVNN 240
|||||

Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLFYEVVNN 266
|||||


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Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 326

Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 4
US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6094

Query Match 100.0%; Score 1760; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRASI 60
Db 27 APTETQPPVTNLSVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRASI 86

Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHNLSYMKCSW 146

Qy 121 LPGRTNSPDNTLYYHRSLEKIHQCENI FREGQYFGCSFDLTAKVQDSSFEQHSVQIMV 180
Db 147 LPGRTNSPDNTLYYHRSLEKIHQCENI FREGQYFGCSFDLTAKVQDSSFEQHSVQIMV 206

Qy 181 KDNAGKIKPSFNI VELTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
Db 207 KDNAGKIKPSFNI VELTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 266

Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 326

Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 5
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
```

```
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-825-561A-82

Query Match 99.1%; Score 1745; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRASI 60
Db 6 APTETQPPVTNLSVSVENLCTVIWTNPPGASNCSLWYFSGDKQDKKIAPETRASI 65

Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHNLSYMKCSW 120
Db 66 EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOQCIWHNLSYMKCSW 125

Qy 121 LPGRTNSPDNTLYYHRSLEKIHQCENI FREGQYFGCSFDLTAKVQDSSFEQHSVQIMV 180
Db 126 LPGRTNSPDNTLYYHRSLEKIHQCENI FREGQYFGCSFDLTAKVQDSSFEQHSVQIMV 185

Qy 181 KDNAGKIKPSFNI VELTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 240
Db 186 KDNAGKIKPSFNI VELTSRVKPPDPHPIKNLSFHNDLLVQWENPQNFISRCCLFYEVVNN 245

Qy 241 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 300
Db 246 SQTETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYDDKL 305

Qy 301 WSNWSQEMSIGKKNST 317
Db 306 WSNWSQEMSIGKKNST 322

RESULT 6
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-30

Query Match 99.1%; Score 1745; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.5e-171;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Query Match	74.7%;	Score	1314.5;	DB 2;	Length	424;			
Best Local Similarity	74.6%;	Pred. No.	5.2e-127;						
Matches	238;	Conservative	35;	Mismatches	45;	Indels	1;	Gaps	
QY	1	APTETQPPVTNLSVSVENLCITVITWNPPEGASSNCSLWYFSGHFGDKDKKIAPETRRSI	60						
DB	25	AATEVQPPVTNLSVSVENLCITVITWNPPEGASSPNCITLRYFHFDDQDKKIAPETHRKE	84						
QY	61	EVPLNERICLVGSGCSSTNESEKPSILVEKCISSPEGDPESAVTELCIWHNLSYNKCSW	120						
DB	85	ELPLDEKICLVGSGCSANESEKPSPLVKKCISPEGDPESAVTELCIWHNLSYNKCSW	144						
QY	121	LPGRNTSDPTNTLYYWHRSLEKIHOCENI FREGQYFGCSFDLTVKYKSSFEQHSVQIMV	180						
DB	145	LPGRNTSDPTHTLYYTSLSLEKSRQCENIYREGQHIACSFKLTKV-BPSFEHQNVQIMV	203						
QY	181	KDNAGKIPSNIVPLTSRVKDPDPHIKNLSFHNDLLVYQWENPQNFISRCLEFYEVEVNN	240						
DB	204	KDNAGKIPSPCKI VSLTSYVKRDPDPHIRHLLKNGALLVQWKNPQFNRSCLTYYEVVNN	263						
QY	241	SQTETHNFFYQEAECNPEFERNVENTSCFVMPVGLPDLTNTVIRVTKNKL CYEDDKL	300						
DB	264	TQTDHNLILEEEDCKQNSDESNNEGTSCFQLPGVLADAVYTVRVRVKTNKLCFCDDNKL	322						
QY	301	WSNWSQEMSIGKKNRSTLY	319						
DB	324	WSDWSEAQSIGKEQNSTFY	342						

RESULT 12

US-09-949-016-8550
 ; Sequence 8550, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8550
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-8550

Query Match	71.9%	Score 1265;	DB 2;	Length 233;
Best Local Similarity	100.0%;	Prod. No. 2.7e-122;		
Matches 231; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	51	KIAPETRRSIEVPLNERICLVGSGCNSNESEKPSILVEKICSPPEGDPESAVTELCQIW	110	
Db	1	KIAPETRRSIEVPLNERICLVGSGCNSNESEKPSILVEKICSPPEGDPESAVTELCQIW	60	
Qy	111	HNLSYMKCSWLPGRNTSPDNTYTLYYMHRSLKIHQCENIFREGQFCGSPDLTKVKDSS	170	
Db	61	HNLSYMKCSWLPGRNTSPDNTYTLYYMHRSLKIHQCENIFREGQFCGSPDLTKVKDSS	120	
Qy	171	FEQHSVQIWMVDNAGKIKPSFNIVPLTSRVPDPDPHINKLSFHNDDLVQWENPQNFISR	230	
Db	121	FEQHSVQIWMVDNAGKIKPSFNIVPLTSRVPDPDPHINKLSFHNDDLVQWENPQNFISR	180	
Qy	231	CLFYEVEVNNSSQTETHNVFYVOEAKCENPBERNVNVENTSCFMVPGVLPTDL	281	
Db	181	CLFYEVEVNNSSQTETHNVFYVOEAKCENPBERNVNVENTSCFMVPGVLPTDL	231	

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RESULT 13
US-09-828-995B-69
; Sequence 69, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND
; FILE REFERENCE: AU-7
; CURRENT APPLICATION NUMBER: US/09/82
; PRIOR FILING DATE: 2001-04-09
; CURRENT APPLICATION NUMBER: 60/195, 874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195, 659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-69

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Query Match 16.8%; Score 296; DB 2; Length 318;
Best Local Similarity 26.9%; Pred. NO. 5.1e-22;
Matches 83; Conservative 52; Mismatches 115; Indels 58; Gaps 15;

Qy	26	WNPP--EGASNCSLWY---FSHPGDKODKKIAP-----ETRRSIEVPLNERICLUQ71
Dd	32	WQPFLPDPNFKECTYIELKTYRNTDSENWKTIITKNLHYKGDFDLNKGIEAKINTLL---88
Qy	72	VGSQCSTNESKPISILVEKCI-SPPEGDPESAVTELOCIWHNLSSYMKCSWLPGFRNTSPDT130
Dd	89	-PAQC--TNGSEVRSWAETTWTSPQGNRETKIQDMDCVYYNQVLVSKWPGMGVHFD146
Qy	131	NYTLYYHRSLEKHOCENIPR-EGVPFGCSDLTVKVDSPFEQHSVQIMKDNAGKIKP189
Dd	147	NYQLFYWYBGLDHBAECTDYLIKVNGKMGCRFPY--LESSDYKDPYICVNGSESQOPINP204
Qy	190	SFNIIVPLTSRVKPDPPPHIKNLSHFN-DDLYYQWENPQNFI-SRCLIFYEVENNSQTE--T245
Dd	205	SYEIFQLQNIKVPMPDDYLSLTVKNSEBINLKNNMWPKGPIPAKCFIYEIEFTEDGTWTWT264
Qy	246	HNVTVQEAECENBEFERNVENTS-----CFMWPGCVLPDILTNTVIRVKTNKLCYEDDK299
Dd	265	TTV-----ENEIQITRTSNESOKLCFLV-----RSKVNIYC--SDDG299
Qy	300	LWSNWSQE307
Dd	300	IWSFWSDE307

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RESULT 14
US-09-828-995B-66
; Sequence 66, Application US/09028995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: AU-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 66
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-66

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Query Match	16.8%;	Score 296;	DB 2;	Length 365;
Best Local Similarity	26.9%;	Pred. No. 6.3e-22;		
Matches	83;	Conservative 52;	Mismatches 115;	Indels 58; Gaps 15;
Qy	26	WNPP--EGASSNSLWY---FSHFGDKQDKKIAP-----ETRSRIEVLNERICLQ	71	
Db	31	WQPLFPDNPKECTIEYELKYRINDSENWKTIIITKNLHYKDGFDLNGKIEAKINTLL---	87	
Qy	72	VGSQCSNTESEKPSILVEKCI--SPPEGDPBSAVTELOCIWHNLSYMKCSMLPGRNTSPDT	130	
Db	88	-PAQC--TNGSEVRSSWAETTYTWSPOGNRETKIQDMDCVYINWQYLVCSPMGVMVHPT	145	
Qy	131	NYTLIYVHRSLKTHQCNIFR--EGQYFGCSFOLTKVKDSSFQHSQIIMVKONAGIKP	189	
Db	146	NYQLFYWYEGLDHSAECTDIYKNGKNWGCRFPY--LESSDYKDFYICVNGSSSQPIRP	203	
Qy	190	SFNIVPLTSRVKPDPPHKNLSFHN--DDLXVQWENPQNFI--SRCLFYEVEVNNSQTE--T	245	
Db	204	SYTFIQLNIVKWPMPDYLSTLVKNSSEINLKNWMPKGPAPAKCFIYEIETEDGTTWVT	263	
Qy	246	HNPFYVOEAKCENPEFRNVENTS-----CFWYPGVLPTLTNIVTRVTKNKLICYEDDK	299	
Db	264	TTV-----ENIQIOTRTSNESQKLCFLY-----RSKNYIYC--SDG	298	

Mon Feb 13 13:13:55 2006

Qy 300 LWSNWSQE 307
Db 299 IWSEWSDE 306

RESULT 15
US-09-828-995B-61
; Sequence 61, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE Igg AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-61

Query Match 16.8%; Score 296; DB 2; Length 386;
Best Local Similarity 26.9%; Pred. No. 6.8e-22;
Matches 83; Conservative 52; Mismatches 115; Indels 58; Gaps 15;
Qy 26 WNP--EGASNCSLWY---FSHFGDKODKXIAP-----ETRRSIEVPLNERICLQ 71
Db 52 WOPLPDPNFKECTIEYELKYRNIDSENWKTITKNLHYKDGFDLNGKIEAKINTLL--- 108
Qy 72 VGSQCSTNESEKPSILVEKCI-SPEGDPESAVTELOCIWHNLGYMKCSWLPGRNTSPDT 130
Db 109 -PAQC-TNGSEVRSSWAETTYTSPQGNRETQIDMDCVYINWQYLVCSWPKGMGVHFD 166
Qy 131 NVTLYYHRSLEKTHOCNIFR-EGQYFGCSFDLTKKVDSSEFQHSVQIMVKDNAGKIKP 189
Db 167 NYQLFYWYEGLDHSAECTDYIKVNGKMGCRPPY--LESSDYKDFYICVNGSSSQPIRP 224
Qy 190 SFNIVPLTSRVKPPDPPIHKNLSFHN-DDLYVQWENPQNF-I-SRCLFYEVVNNSQTE--T 245
Db 225 SYFIFQLQNIWKMPDYLSTLVKNSBINKWNPKGPIPAKCFIYEIEFTEDGTTWVT 284
Qy 246 HNVFYVQAKENPEFRNVENTS-----CFWVPGVLPTINTVRIKTNKLCYEDDK 299
Db 285 TTV-----ENEIQTITSNESQKLCFLV-----RSKNVIYC-SDDG 319
Qy 300 LWSNWSQE 307
Db 320 IWSEWSDE 327

Search completed: February 8, 2006, 22:10:45
Job time : 27.5039 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 86.7655 Seconds
(without alignment)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

Sequence: 1 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFSGDKQDKKIAPETRRSI 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1760	100.0	427	4	US-10-671-697-9
2	1760	100.0	427	5	US-10-850-270-4
3	1760	100.0	427	6	US-11-067-251-3
4	1745	99.1	322	3	US-09-825-561A-82
5	1745	99.1	322	5	US-10-872-087-82
6	1745	99.1	664	5	US-10-850-270-10
7	1745	99.1	776	3	US-09-935-868-36
8	1745	99.1	780	3	US-09-935-868-34
9	1745	99.1	784	3	US-09-313-942-30
10	1745	99.1	784	3	US-09-935-868-30
11	1745	99.1	784	4	US-10-287-035-30
12	1745	99.1	784	4	US-10-282-162-30
13	1745	99.1	784	6	US-11-134-114-30
14	1745	99.1	793	3	US-09-313-942-32
15	1745	99.1	793	3	US-09-935-868-32
16	1745	99.1	793	4	US-10-287-035-32
17	1745	99.1	793	4	US-10-282-162-32
18	1745	99.1	793	6	US-11-134-114-32
19	1742	99.0	426	4	US-10-036-568-4
20	1736	98.6	776	3	US-09-935-868-44
21	1736	98.6	776	6	US-11-067-251-8
22	1736	98.6	776	6	US-11-067-251-10
23	1736	98.6	776	6	US-11-067-251-12
24	1736	98.6	776	6	US-11-067-251-14
25	1736	98.6	776	6	US-11-067-251-16
26	1736	98.6	778	3	US-09-935-868-46
27	1736	98.6	778	4	US-10-287-035-46

28	1736	98.6	778	4	US-10-287-035-60	Sequence 60, Appl
29	1736	98.6	780	3	US-09-935-868-42	Sequence 42, Appl
30	1736	98.6	782	3	US-09-935-868-48	Sequence 48, Appl
31	1735	98.6	776	3	US-09-935-868-40	Sequence 40, Appl
32	1735	98.6	778	3	US-09-935-868-50	Sequence 50, Appl
33	1735	98.6	778	4	US-10-287-035-50	Sequence 50, Appl
34	1735	98.6	778	4	US-10-287-035-56	Sequence 56, Appl
35	1735	98.6	780	3	US-09-935-868-38	Sequence 38, Appl
36	1735	98.6	782	3	US-09-935-868-52	Sequence 52, Appl
37	1731.5	98.4	780	4	US-10-287-035-34	Sequence 34, Appl
38	1729	98.2	776	4	US-10-287-035-40	Sequence 40, Appl
39	1722.5	97.9	780	4	US-10-287-035-42	Sequence 42, Appl
40	1722.5	97.9	782	4	US-10-287-035-48	Sequence 48, Appl
41	1722.5	97.9	782	4	US-10-287-035-54	Sequence 54, Appl
42	1721.5	97.8	780	4	US-10-287-035-38	Sequence 38, Appl
43	1721.5	97.8	782	4	US-10-287-035-52	Sequence 52, Appl
44	1721.5	97.8	782	4	US-10-287-035-58	Sequence 58, Appl
45	1720	97.7	776	4	US-10-287-035-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9

Query Match 100.0%; Score 1760; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFSGDKQDKKIAPETRRSI 60
DB 27 APTETQPPVTNLSVSVENLCTVIWNPPEGSSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVGSCQSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 120

Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 2

US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EH
; CURRENT APPLICATION NUMBER: US/10/850,270
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human
US-10-850-270-4

Query Match 100.0%; Score 1760; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQKKIAPETRRSI 60
Db 27 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 3

US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3

Query Match 100.0%; Score 1760; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQKKIAPETRRSI 60
Db 27 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSCSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSPHNDLLYQWENPQNFISRCLFYEVVNN 266
Qy 241 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 300
Db 267 SQTEHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVTKNKLCEYDDKL 326
Qy 301 WSNWSQEMSIGKKNSTLYI 320
Db 327 WSNWSQEMSIGKKNSTLYI 346

RESULT 4

US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05

		PRIOR APPLICATION NUMBER: US 60/222,121			
		PRIOR FILING DATE: 2000-07-28			
		NUMBER OF SEQ ID NOS: 86			
		SOFTWARE: FastSeq for Windows Version 3.0			
		SEQ ID NO 82			
		LENGTH: 322			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-825-561A-82			
		Query Match 99.1%; Score 1745; DB 3; Length 322;			
		Best Local Similarity 100.0%; Pred. No. 3.3e-147;			
		Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFPGDKQDKKIAPETR	RSI	60	
Db	6	APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFPGDKQDKKIAPETR	RSI	65	
Qy	61	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		120	
Db	66	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		125	
Qy	121	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		180	
Db	126	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		185	
Qy	181	KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	240	
Db	186	KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	245	
Qy	241	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDILTNTVIRVKTNKL	CYEDDKL	300	
Db	246	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDILTNTVIRVKTNKL	CYEDDKL	305	
Qy	301	WSNSQEMSIGKKRNST	317		
Db	306	WSNSQEMSIGKKRNST	322		
RESULT 6					
US-10-850-270-10					
; Sequence 10, Application US/10850270					
; Publication No. US20050058645A1					
; GENERAL INFORMATION:					
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)					
; APPLICANT: Dunlop, Felicity (US only)					
; APPLICANT: Baca, Manuel (US only)					
; APPLICANT: Nash, Andrew (US only)					
; APPLICANT: Fabri, Louis (US only)					
; TITLE OF INVENTION: Novel peptides					
; FILE REFERENCE: 12175890/EH					
; CURRENT APPLICATION NUMBER: US/10/850,270					
; CURRENT FILING DATE: 2004-05-20					
; PRIOR APPLICATION NUMBER: AU P51301					
; PRIOR FILING DATE: 2002-03-22					
; PRIOR APPLICATION NUMBER: AU 2003900437					
; PRIOR FILING DATE: 2003-02-03					
; NUMBER OF SEQ ID NOS: 28					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 10					
; LENGTH: 664					
; TYPE: PRT					
; ORGANISM: human					
US-10-850-270-10					
		Query Match 99.1%; Score 1745; DB 5; Length 664;			
		Best Local Similarity 100.0%; Pred. No. 8.6e-147;			
		Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFPGDKQDKKIAPETR	RSI	60	
Db	45	APTETQPPVTNLSVSVENLCTVIWTPNPPGASNCSLWYFSHFPGDKQDKKIAPETR	RSI	104	
Qy	61	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		120	
Db	105	EVPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW		164	
Qy	121	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		180	
Db	165	LPGRNTSPDNTYTLYYWHSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV		224	
Qy	181	KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	240	
Db	225	KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYQWENPQNFISRCLFYEV	VNN	284	
Qy	241	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDILTNTVIRVKTNKL	CYEDDKL	300	
Db	285	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDILTNTVIRVKTNKL	CYEDDKL	344	

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QY 301 WSNWSQEMSIGKGRNST 317
Db 345 WSNWSQEMSIGKGRNST 361
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RESULT 7
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36

Query Match 99.1%; Score 1745; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 60
Db 232 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 291
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QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 292 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 351
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QY 121 LPRGNTSPDNTNLTYYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 352 LPRGNTSPDNTNLTYYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 411
|||||

QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVEVNN 240
Db 412 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVEVNN 471
|||||

QY 241 SQTETHNVFYVQEAACENPFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 472 SQTETHNVFYVQEAACENPFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 531
|||||

QY 301 WSNWSQEMSIGKGRNST 317
Db 532 WSNWSQEMSIGKGRNST 548
|||||

RESULT 8
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-34

Query Match 99.1%; Score 1745; DB 3; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFHFGDKQDKKIAPETRRSI 298
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QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 358
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QY 121 LPRGNTSPDNTNLTYYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 359 LPRGNTSPDNTNLTYYWHRSLKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
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QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNDDLYVOWENPQNFISRCLFYEVEVNN 478
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Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 538

Qy 301 WSNWSQEMSGKKRNST 317
Db 539 WSNWSQEMSGKKRNST 555

RESULT 10
US-10-935-868-30
; Sequence 30, Application US/09935868
; Publication No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-935-868-30

Query Match 99.1%; Score 1745; DB 3; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 298

Qy 61 EVPLNERICLQVGSQCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLQVGSQCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 358

Qy 121 LPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 180
Db 359 LPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 418

Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWNPQNFISRCLFYEEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWNPQNFISRCLFYEEVEVNN 478

Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 538

Qy 301 WSNWSQEMSGKKRNST 317
Db 539 WSNWSQEMSGKKRNST 555

RESULT 11
US-10-287-035-30
; Sequence 30, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
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; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-30

Query Match 99.1%; Score 1745; DB 4; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 298

Qy 61 EVPLNERICLQVGSQCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLQVGSQCSNTESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 358

Qy 121 LPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 180
Db 359 LPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTAKVDSSFEQHSVQIMV 418

Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWNPQNFISRCLFYEEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLLYVQWNPQNFISRCLFYEEVEVNN 478

Qy 241 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 300
Db 479 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTRVIRVKTNKLCEYDDKL 538

Qy 301 WSNWSQEMSGKKRNST 317
Db 539 WSNWSQEMSGKKRNST 555

RESULT 12
US-10-282-162-30
; Sequence 30, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30

Query Match 99.1%; Score 1745; DB 4; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFHFGDKODKKIAPETRRSI 298
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QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 358
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 359 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 478
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 300
Db 479 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 538
QY 301 WSNWSQEMSIGKKNST 317
Db 539 WSNWSQEMSIGKKNST 555

RESULT 13
US-11-134-114-30
; Sequence 30, Application US/11134114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203CI
; CURRENT APPLICATION NUMBER: US/11/134,114
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784'
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-30

Query Match 99.1%; Score 1745; DB 6; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 298
QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 358
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 359 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 478
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 300
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
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Db 479 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 538
QY 301 WSNWSQEMSIGKKNST 317
Db 539 WSNWSQEMSIGKKNST 555

RESULT 14
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match 99.1%; Score 1745; DB 3; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.1e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 27 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHDDLQVQWENPQNFISRCLFYVEVNN 266
QY 241 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 300
Db 267 SQTETHNVFYQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKLCEYDDKL 326
QY 301 WSNWSQEMSIGKKNST 317
Db 327 WSNWSQEMSIGKKNST 343

RESULT 15
US-09-935-868-32
; Sequence 32, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-32

Query Match      99.1%; Score 1745; DB 3; Length 793;
Best Local Similarity 100.0%; Pred. No. 11e-146;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFSHFQDKQDKKIAPETRRSI 60
Db  1  |||||||
Qy 27  APTETQPPVTNLSVSVENLCTVIWTNPPPEGASNCSLWYFSHFQDKQDKKIAPETRRSI 86
Db 27  |||||||
Qy 61  EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 120
Db 61  |||||||
Qy 87  EVPLNERICLVGSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 146
Db 87  |||||||
Qy 121 LPGRNTSPDNTYTLYYWHSLEKIHQENI FREGQYFGCSFDLT KVXDSSFEQHSVQIMV 180
Db 121 |||||||
Qy 147 LPGRNTSPDNTYTLYYWHSLEKIHQENI FREGQYFGCSFDLT KVXDSSFEQHSVQIMV 206
Db 147 |||||||
Qy 181 KDNAGKIKPSFNI VPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 240
Db 181 |||||||
Qy 207 KDNAGKIKPSFNI VPLTSRVKPDPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
Db 207 |||||||
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVRI RVKTNKLCYEDDKL 300
Db 241 |||||||
Qy 267 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVRI RVKTNKLCYEDDKL 326
Db 267 |||||||
Qy 301 WSNWSQEMSIGKKRNST 317
Db 301 |||||||
Qy 327 WSNWSQEMSIGKKRNST 343
Db 327 |||||||
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 ; Search time 6.97472 Seconds
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Title: US-10-036-568A-4_COPY_26_345

Perfect score: 1760

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/US05 NEW PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1760	100.0	427	US-11-185-230-4	Sequence 4, Appli
2	1305.5	74.2	424	US-11-185-230-6	Sequence 6, Appli
3	284	16.1	378	US/11/185	Sequence 12, Appli
4	284	16.1	380	US-10-989-313-4	Sequence 4, Appli
5	284	16.1	380	US-11-185-230-2	Sequence 2, Appli
6	278	15.8	383	US-10-989-313-2	Sequence 2, Appli
7	230	13.1	313	US-11-193-512-106	Sequence 106, App
8	230	13.1	420	US-11-185-230-5	Sequence 5, Appli
9	181.5	10.3	341	US-10-511-722-21	Sequence 21, Appli
10	181.5	10.3	357	US-10-511-722-20	Sequence 20, Appli
11	181.5	10.3	369	US-11-105-268-60	Sequence 60, Appli
12	178.5	10.1	411	US-11-075-351-47	Sequence 47, Appli
13	168.5	9.6	329	US-10-995-561-694	Sequence 694, App
14	168.5	9.6	646	US-10-995-561-695	Sequence 695, App
15	168.5	9.6	708	US-10-636-320-2	Sequence 2, Appli
16	168.5	9.6	918	US-10-995-561-696	Sequence 696, App
17	146	8.3	897	US-11-124-367A-449	Sequence 449, App
18	146	8.3	897	US-11-124-367A-451	Sequence 451, App
19	144	8.2	903	US-11-124-367A-450	Sequence 450, App
20	110.5	6.3	825	US-10-995-561-679	Sequence 679, App
21	110.5	6.3	825	US-11-124-367A-469	Sequence 469, App
22	110.5	6.3	852	US-11-104-923A-5	Sequence 5, Appli
23	107	6.1	631	US-10-813-646-22	Sequence 22, Appli
24	102.5	5.8	1905	US-10-877-346-44	Sequence 44, Appli
25	101.5	5.8	896	US-11-192-219-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-11-185-230-4

; Sequence 4, Application US/11185230

; Publication No. US20050282216A1

; GENERAL INFORMATION:

; APPLICANT: Caput, Daniel

; APPLICANT: Ferrara, Pascual

; APPLICANT: Laurent, Patrick

; APPLICANT: Vita, Natalio

; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity

; FILE REFERENCE: IVD924 US CNT 1

; CURRENT APPLICATION NUMBER: US/11/185.230

; CURRENT FILING DATE: 2005-07-18

; PRIOR APPLICATION NUMBER: PCT/FR96/01756

; PRIOR FILING DATE: 1996-11-07

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 4

; LENGTH: 427

; TYPE: PRT 3

; ORGANISM: Homo sapiens

; FEATURE:

US-11-185-230-4

Query Match	100.0%;	Score 1760;	DB 7;	Length 427;
Best Local Similarity	100.0%;	Pred. No. 5e-153;		
Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	APTETQPPVTNLSVSVENLCTVITWNPPEGASSNCSLWYFSHFQDKQDKKIAPETRRSI	60	
Db	27	APTETQPPVTNLSVSVENLCTVITWNPPEGASSNCSLWYFSHFQDKQDKKIAPETRRSI	86	
QY	61	EVPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW	120	
Db	87	EVPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELQCIWHNLSYMKCSW	146	
QY	121	LPGRNTSPDTNTVTLTYWHSRLEKIHQCENIFREGQYFGCSFDLTVKYQDSSFQHSVQIMV	180	
Db	147	LPGRNTSPDTNTVTLTYWHSRLEKIHQCENIFREGQYFGCSFDLTVKYQDSSFQHSVQIMV	206	
QY	181	KDNACKIKPSFNIVELTSRVKPDPPHINKNLSFNHNDLLYQWENPNQFISRCIFYEVEVNN	240	
Db	207	KDNACKIKPSFNIVELTSRVKPDPPHINKNLSFNHNDLLYQWENPNQFISRCIFYEVEVNN	266	
QY	241	SQTEHNTVYVQEAECENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL	300	
Db	267	SQTEHNTVYVQEAECENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL	326	

Qy 301 WSNWSQEMSGKKRNSTLYI 320
Db 327 WSNWSQEMSGKKRNSTLYI 346

RESULT 2

US-11-185-230-6

; Sequence 6, Application US/11185230
; Publication No. US20050282216A1

; GENERAL INFORMATION:

; APPLICANT: Caput, Daniel

; APPLICANT: Ferrara, Pascual

; APPLICANT: Laurent, Patrick

; APPLICANT: Vita, Natalio

; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity

; FILE REFERENCE: IVD924 US CNT 1

; CURRENT APPLICATION NUMBER: US/11/185,230

; CURRENT FILING DATE: 2005-07-18

; PRIOR APPLICATION NUMBER: PCT/FR96/01756

; PRIOR FILING DATE: 1996-11-07

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 424

; TYPE: PRT 3

; ORGANISM: Mus musculus

; FEATURE:

US-11-185-230-6

Query Match 74.2%; Score 1305.5; DB 7; Length 424;
Best Local Similarity 74.3%; Pred. No. 1.3e-111; Indels 1; Gaps 1;
Matches 237; Conservative 35; Mismatches 46;

Qy 1 APTETQPPVTLNLSVSVENLCTVIWTWNPPEGASNSCSLWYFHFHGDQDKKIAPETRRSI 60
Db 25 AATEVQPPVTLNLSVSVENLCTVIWTWNPPEGASPNCTLRVYFHFDDQDKKIAPETHRKE 84
Qy 61 EVPLNERICLQVGSQCSSTNESEKPSILVEKCIIPPEDGESAVTELOCIWHNLSYMKCSW 120
Db 85 ELPLDERICLQVGSQCSANSEKPSPLVKKCIIPPEDGESAVTELOCIWHNLSYMKCSW 144
Qy 121 LPCRNTSPDNTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTQVKDSSFEQHSVQIMV 180
Db 145 LPCRNTSPDNTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTQVKDSSFEQHSVQIMV 203
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLQVQENPQNFISRCIFYEVEVNN 240
Db 204 KDNAGKIRPCKIVSLTSYVKPDPPIKHLKNGALLVQWKNPQNSRCLTYEVEVNN 263
Qy 241 SQETHNVFVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 300
Db 264 TOTDRHNLVEEDKCNQSDRNMEGTSCFQLPGVLADAVYTVRVKTKNKLCEYEDDKL 323
Qy 301 WSNWSQEMSGKKRNSTLYI 319
Db 324 WSDWSEAQSGKQNSTFY 342

RESULT 3

US/11/185

; Sequence 12, Application US/11185230
; Publication No. US20050282216A1

; GENERAL INFORMATION:

; APPLICANT: Caput, Daniel

; APPLICANT: Ferrara, Pascual

; APPLICANT: Laurent, Patrick

; APPLICANT: Vita, Natalio

; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity

; FILE REFERENCE: IVD924 US CNT 1

; CURRENT APPLICATION NUMBER: US/11/185,230

; CURRENT FILING DATE: 2005-07-18

; PRIOR APPLICATION NUMBER: PCT/FR96/01756

; PRIOR FILING DATE: 1996-11-07

; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12

; LENGTH: 378

; TYPE: PRT 3

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted

US/11/185,230-12

Query Match 16.1%; Score 284; DB 7; Length 378;
Best Local Similarity 28.7%; Pred. No. 1.3e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

Qy 26 WNPPEGAS--SNCSLWYFHFHGDQDKKIAPETRRSI-----EVPLNERICLQVGS 74
Db 53 WQPPLSLDHPKECTVEY-----ELKYRNIGSETWTKIITKNLHYKQDFDLNKGIEAKIHT 107

Qy 75 ----QCSTNESEKPSILVEKC--ISPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC--TNGSEVOSSWAETTYWIS--PQGIPEPKVQDMDCVYVNWQYLLCSWPKPGIGVLL 165

Qy 129 DTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTQVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTNYNLFYWYEGLDHALQCVDIYKADQONIGCRFPYLEASD--YKDFYICVNGSSSENKPI 223

Qy 188 KPSFNIVPLTSRVKPPPHIKNLSFHNDDLQVQENPQNFISRCIFYEVEVNNST 243
Db 224 RSYFTFQLQNIYVKPLPP--VYLTFTRSSCEIKLWMSIPLGPIPARCFDYEIEIREDDT 281

Qy 244 ETHNVFVQAEKCNPEFERNVENTS---CFMYPGVLPDTLNTVIRVTKNKLCEYEDDKL 300
Db 282 T-----LVATVENETTYTLTKTTNETRQLCFVW-----RSKNIIYC--SDG 321

Qy 301 WSNWSQ 307

Db 322 WSEWSDK 328

RESULT 4

US-10-989-313-4

; Sequence 4, Application US/10989313

; Publication No. US20050277126A1

; GENERAL INFORMATION:

; APPLICANT: Collins, Mary

; APPLICANT: Donaldson, Debra

; APPLICANT: Fitz, Lora

; APPLICANT: Neben, Tamlyn

; APPLICANT: Whitters, Matthew

; APPLICANT: Wood, Clive

; APPLICANT: Wills-Karp, Marsha

; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: Cytokine Receptor Chain

; FILE REFERENCE: GI 5268A

; CURRENT APPLICATION NUMBER: US/10/989,313

; CURRENT FILING DATE: 2004-11-15

; PRIOR APPLICATION NUMBER: US/09/868,123

; PRIOR FILING DATE: 2002-04-02

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 380

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-989-313-4

Query Match 16.1%; Score 284; DB 6; Length 380;

Best Local Similarity 28.7%; Pred. No. 1.4e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

Qy 26 WNPPEGAS--SNCSLWYFHFHGDQDKKIAPETRRSI-----EVPLNERICLQVGS 74
Db 53 WQPPLSLDHPKECTVEY-----ELKYRNIGSETWTKIITKNLHYKQDFDLNKGIEAKIHT 107


```
QY 75 ----QCSTNESEKPSILVEK--ISPPEGDPSAVTELCQIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC-TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYINWQYLCSWKEGIGVLL 165
QY 129 DTNTYTYWHRSLKIHQC-ENIFREGQYFGCSFDLTQVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTYNLFWYEGDLHALQCDVYIKADQGNIGCRFPYLEASD--YKDFYICVNGSSSENKPI 223
QY 188 KPSFNIVPLTSRVKDPDPHIIKNLSFHDND---DLVQWENPQNFI-SRCLFYEVEVNSQT 243
Db 224 RSSYFTFQLOQIVKPLPP--VYLTFRESSCEIKLWSIPLGPICPARCFDYEIREDDT 281
QY 244 ETHNVFYVQEAKECENPEPERNVENTS---CFMVPGLVPLDTLNTVIRVKTNKLVEYDDKL 300
Db 282 T-----LVTATVENETTYLTKTTNETROLQCFV-----RSKNIYC-SDDGI 321
QY 301 WSNWSOE 307
Db 322 WSEWSDK 328

RESULT 5
US-11-185-230-2
; Sequence 2, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: INV924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-2

Query Match 16.1%; Score 284; DB 7; Length 380;
Best Local Similarity 28.7%; Pred. No. 1.4e-18;
Matches 88; Conservative 47; Mismatches 116; Indels 56; Gaps 16;

QY 26 WNPPEGAS--SNCSLWYFSHFGDKQDKKIAPETRSI-----EVLNERICLQVGS 74
Db 53 WQPLSLDHFKECTVEY-----ELKRYNIGSETWKTITKNLHYKDGFDLNKGIEAKIHT 107
QY 75 ----QCSTNESEKPSILVEK--ISPPEGDPSAVTELCQIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPWQC-TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYINWQYLCSWKEGIGVLL 165
QY 129 DTNTYTYWHRSLKIHQC-ENIFREGQYFGCSFDLTQVKDSSFEQHSVQIMVKDNAGKI 187
Db 166 DTYNLFWYEGDLHALQCDVYIKADQGNIGCRFPYLEASD--YKDFYICVNGSSSENKPI 223
QY 188 KPSFNIVPLTSRVKDPDPHIIKNLSFHDND---DLVQWENPQNFI-SRCLFYEVEVNSQT 243
Db 224 RSSYFTFQLOQIVKPLPP--VYLTFRESSCEIKLWSIPLGPICPARCFDYEIREDDT 281
QY 244 ETHNVFYVQEAKECENPEPERNVENTS---CFMVPGLVPLDTLNTVIRVKTNKLVEYDDKL 300
Db 282 T-----LVTATVENETTYLTKTTNETROLQCFV-----RSKNIYC-SDDGI 321
QY 301 WSNWSOE 307
Db 322 WSEWSDK 328
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RESULT 6

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US-10-989-313-2
; Sequence 2, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-989-313-2
```

Query Match 15.8%; Score 278; DB 6; Length 383;
Best Local Similarity 26.0%; Pred. No. 4.8e-18;
Matches 77; Conservative 47; Mismatches 138; Indels 34; Gaps 11;

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QY 26 WNP-----EGASNCSLWYFSHFGDKQDKKIAPETRSIEVPLNE----RICLQVGSQ 75
Db 47 WKPFWIEKFKGCTLEYELKYRNVDSWSWKTITRNLIYKDGFDLNKGIEGKIRTHLSEH 106
QY 76 CSTNESEKPSILVEKCSIS-PPEGDPSAVTELCQIWHNLSYMKCSWLPGRNTSPDTNTYL 134
Db 107 C-TNGSEVQSSWAETTYWIS-DEGSLTKIQDKMCLYINWQYLVCSSWKFGKTVSDNTYTM 165
QY 135 YYWHRSLKIHQCENIFR-EGQYFGCSFDLTQVKDSSFEQHSVQIMVKDNAGKI KPSFNI 193
Db 166 FFWYEGDLHALQCADYLQHDENKVGCK--LSNLSSDYKDFPICVNGSSKLEPIRSSYTV 223
QY 194 VPLTSRVKDPDPHIIKNLSFHDND-DLVQWENPQNFI-SRCLFYEVEVNSQTETNVFV 251
Db 224 FQLOQIVKPLPEPEFLHISVENSIDIRMKWSTPGGIPPRCYTYEIVIREDDISWESATDK 283
QY 252 QEAKECENPEPERNVENTS CFMVPGLVPLDTLNTVIRVKTNKLVEYDDKLWNSWSOE 307
Db 284 NDMKLK---RANESDLCFV-----RCKNIYC-ADGGIWSMSEE 322

RESULT 7
US-11-193-512-106
; Sequence 106, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, Nobuo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-AUG-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-11-193-512-106

Query Match      13.1%; Score 230; DB 7; Length 313;
Best Local Similarity 24.8%; Pred. No. 8.9e-14;
Matches 82; Conservative 51; Mismatches 145; Indels 52; Gaps 14;

Qy 7 PPVTNLVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 65
Db 12 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRVNLEY-----QVKINAPK-EDDYETRI 62
Qy 66 ERICLQV-----GSQCSTNESEKPSILVEKCI-----PPEGDPESAVTELQCIWHNL--- 113
Db 63 ESKCVTLHKGFSAVRTLQNDHSLASSWASAEHLHAPPGSPGTSVVNLTCTTTNTEDN 122
Qy 114 -----SY-----MKCSWLPGRNTSPDTNTLYYHRSLEKIHQCENIPRE--GOYFGCSFDL 163
Db 123 YSLRSYQVSLHCTWLVTGDPEDTQFLYRYGWSWTE--ECQEYSKDTLGRNIACWFR 180
Qy 164 TKVKDSSFQHSQVIMVKDNAGIKPFSFNIVPLTSRVKPPPHIKNLSFNDLDLYQWEN 223
Db 181 TFILSKGRDMLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIGTRLSIQWEK 240
Qy 224 PQN-FISRCFLFYEVVNNSTQETHNVFYQBAKCEPNERNVNVENTSCFMVPGVLPDTLN 282
Db 241 PVSAPFTHCFDYEYVKIHTNRG-----YLQIEKLTMTNAFISIIDLISKY----- 284
Qy 283 TVRIRVTKNLKCYEDDDKLSNWSQEMSIGK 312
Db 285 DVQVRAAVSSMCREAG-LWSEWSQPIYVGK 313

RESULT 8
US-11-185-230-5
; Sequence 5, Application US/11185230
; Publication No. US2005028216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
```

```
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 420
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-5

Query Match      13.1%; Score 230; DB 7; Length 420;
Best Local Similarity 24.4%; Pred. No. 1.3e-13;
Matches 82; Conservative 52; Mismatches 150; Indels 52; Gaps 14;

Qy 7 PPVTNLVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 65
Db 32 PPV-NFTIKVTGLAQVLLQWKPNPDQEQRVNLEY-----QVKINAPK-EDDYETRI 82
Qy 66 ERICLQV-----GSQCSTNESEKPSILVEKCI-----PPEGDPESAVTELQCIWHNL--- 113
Db 83 ESKCVTLHKGFSAVRTLQNDHSLASSWASAEHLHAPPGSPGTSIVNLTCTTTNTEDN 142
Qy 114 -----SY-----MKCSWLPGRNTSPDTNTLYYHRSLEKIHQCENIPRE--GOYFGCSFDL 163
Db 143 YSLRSYQVSLHCTWLVTGDPEDTQFLYRYGWSWTE--ECQEYSKDTLGRNIACWFR 200
Qy 164 TKVKDSSFQHSQVIMVKDNAGIKPFSFNIVPLTSRVKPPPHIKNLSFNDLDLYQWEN 223
Db 201 TFILSKGRDMLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIGTRLSIQWEK 260
Qy 224 PQN-FISRCFLFYEVVNNSTQETHNVFYQBAKCEPNERNVNVENTSCFMVPGVLPDTLN 282
Db 261 PVSAPFTHCFDYEYVKIHTNRG-----YLQIEKLTMTNAFISIIDLISKY----- 304
Qy 283 TVRIRVTKNLKCYEDDDKLSNWSQEMSIGKRNSTL 318
Db 305 DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPL 339

RESULT 9
US-10-511-722-21
; Sequence 21, Application US/10511722
; Publication No. US2005028714A1
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd.
; APPLICANT: Wallach, David
; APPLICANT: Shmushkovich, Taisia
; APPLICANT: Ramakrishnan, Parameswaran
; TITLE OF INVENTION: Derivatives of the IL-2 receptor Gamma chain, their preparation and
; FILE REFERENCE: 530
; CURRENT APPLICATION NUMBER: US/10/511,722
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 149217
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 152183
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-722-21

Query Match      10.3%; Score 181.5; DB 6; Length 341;
Best Local Similarity 26.8%; Pred. No. 2.6e-09;
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; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-60

Query Match          10.3%; Score 181.5; DB 7; Length 369;
Best Local Similarity 26.8%; Pred. No. 2.9e-09;
Matches 61; Conservative 39; Mismatches 87; Indels 41; Gaps 12;

QY 105 ELQCIWHNLISYMKCSWLPGRNTSPDNTYLTLYWHRSL--EKIHQCEN-IFREGQYFGCSF 161
DB 59 EQVCFVFNVEYMNCTWNSSSEQP-TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGC-- 115

QY 162 DLTKVKDSSPEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIHKNSLFH---NDDLY 218
DB 116 QLQKKEIHLQYTFVQL--QDPREPRQATQMLKQLNLVIPWAP--ENLTLHKLSQLE 171

QY 219 VQWENPQNTISRL-----FYEVEVNSQTEHNVFVQEAACENPFRNVENTSCFMVP 274
DB 172 LNWNN--RFLNHGCHLHVQYRTDWDHSWT-----EQSDVYRHKFSLP 211

QY 275 GVLPDTLNTRIRVKTNKLCYEDDKLWSNQMSIG---KKRNSTLY 319
DB 212 SVDGQKRYTFRVRSRENPLC-GSAQHSEWSHPHIGWNTSKENPPLF 258

RESULT 12
US-11-075-351-47
; Sequence 47, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-11-075-351-47

Query Match          10.1%; Score 178.5; DB 7; Length 411;
Best Local Similarity 26.5%; Pred. No. 6.1e-09;
Matches 60; Conservative 39; Mismatches 86; Indels 41; Gaps 12;

QY 105 ELQCIWHNLISYMKCSWLPGRNTSPDNTYLTLYWHRSL--EKIHQCEN-IFREGQYFGCSF 161
DB 72 EQVCFVFNVEYMNCTWNSSSEQP-TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGC-- 128

QY 162 DLTKVKDSSPEQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIHKNSLFH---NDDLY 218
DB 129 QLQKKEIHLQYTFVQL--QDPREPRQATQMLKQLNLVIPWAP--ENLTLHKLSQLE 184

QY 219 VQWENPQNTISRL-----FYEVEVNSQTEHNVFVQEAACENPFRNVENTSCFMVP 274
DB 185 LNWNN--RFLNHGCHLHVQYRTDWDHSWT-----EQSDVYRHKFSLP 224

QY 275 GVLPDTLNTRIRVKTNKLCYEDDKLWSNQMSIG---KKRNST 317

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Db 225 SVDGQKRYTFRVRSRNPCLC-GSAQHWSWSHPHGWGNTSKENG 269

RESULT 13

US-10-995-561-694

Sequence 694, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT FILING DATE: 2004-11-24

CURRENT APPLICATION NUMBER: US/10/995,561

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 694

LENGTH: 329

TYPE: PRT

ORGANISM: Homo sapiens

US-10-995-561-694

Query Match 9.6%; Score 168.5; DB 6; Length 329;

Best Local Similarity 25.3%; Pred. No. 3.8e-08;

Mismatches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

QY 6 QPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFG-DKODKKIAPETRSIEVPL 64

DB 34 ESPVQLHNSFTAVCVLKEKMDYFHVNAVYIVWKTNHTPTPKQYTIINRTASSVTFTD 93

QY 65 NERICLVQSGQSTNESEKPSILVEKICIS--PPEGDPESAVTELCQIWHNLSYMKCSWLP 122

DB 94 IASLNIQLTCNLITFGQLEQNQVYGITIIISGLPPE-KPKN----LSCIVNEGKKWRCWDG 148

QY 123 GRNTSPDPTNYTL--YYWHRSLKIHOCENIFREGQVFGCSFDLTQKVKOSSFQHSVQIMVK 181

DB 149 GRETHLETNFTLKSEW--ATHKFADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201

QY 182 DNAGKI-KPSFNIVPLTSRVKDPDPHKNLSFHNDD-----LYVQWENPQNFISRCLEYE 235

DB 202 NALGKVTSDHINFPDPV-YKVKPNPPH--NLSVINSEELSSILKLTWTNTPSIKSVIILKYN 258

QY 236 VEVNNSQTETHNVFVYQEAKECNPEFERNVENTSCFMPVPGVLPDTLNTVIRVKTNKLKY 295

DB 259 IQYRTKDASTWS-----QIPP-EDTASTRSFTVQDLKPTTEYVFRIR-----CM 302

QY 296 EDD--KLMSNWSQEMS 309

DB 303 KEDGKGYSWDSWEAS 318

RESULT 14

US-10-995-561-695

Sequence 695, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT FILING DATE: 2004-11-24

CURRENT APPLICATION NUMBER: US/10/995,561

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 695

LENGTH: 646

TYPE: PRT

ORGANISM: Homo sapiens

US-10-995-561-695

Query Match 9.6%; Score 168.5; DB 6; Length 646;

Best Local Similarity 25.3%; Pred. No. 8.6e-08;

Mismatches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

QY 6 QPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFG-DKODKKIAPETRSIEVPL 64

DB 34 ESPVQLHNSFTAVCVLKEKMDYFHVNAVYIVWKTNHTPTPKQYTIINRTASSVTFTD 93

QY 65 NERICLVQSGQSTNESEKPSILVEKICIS--PPEGDPESAVTELCQIWHNLSYMKCSWLP 122

DB 94 IASLNIQLTCNLITFGQLEQNQVYGITIIISGLPPE-KPKN----LSCIVNEGKKWRCWDG 148

QY 123 GRNTSPDPTNYTL--YYWHRSLKIHOCENIFREGQVFGCSFDLTQKVKOSSFQHSVQIMVK 181

DB 149 GRETHLETNFTLKSEW--ATHKFADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201

QY 182 DNAGKI-KPSFNIVPLTSRVKDPDPHKNLSFHNDD-----LYVQWENPQNFISRCLEYE 235

DB 202 NALGKVTSDHINFPDPV-YKVKPNPPH--NLSVINSEELSSILKLTWTNTPSIKSVIILKYN 258

QY 236 VEVNNSQTETHNVFVYQEAKECNPEFERNVENTSCFMPVPGVLPDTLNTVIRVKTNKLKY 295

DB 259 IQYRTKDASTWS-----QIPP-EDTASTRSFTVQDLKPTTEYVFRIR-----CM 302

QY 296 EDD--KLMSNWSQEMS 309

DB 303 KEDGKGYSWDSWEAS 318

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/636,320

FILING DATE: 06-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/313,135

FILING DATE: 2002-12-06

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

APPLICATION NUMBER: US/09/058,264

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

```

;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 708 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-636-320-2

Query Match      9.6%; Score 168.5; DB 6; Length 708;
Best Local Similarity 25.3%; Pred. No. 9.6e-08;
Matches 80; Conservative 45; Mismatches 148; Indels 43; Gaps 16;

Qy  6 QPPVTNLSVSVENLCTVIWTPNPPGASSNCSLWYFSHFG-DKQDKKIAPETRRSIEVPL 64
Db  34 ESPVVQLHSNFTAVCVLKEKCMDFHVNANYIVMKNHTIPKEQYTIINRTASSVTFTD 93

Qy  65 NERICLVGSGCSTNESEKPSILVEKCIS--PREGDPESAATELQCIWHNLSYMKCSWLP 122
Db  94 IASLNIQTNCNLTGQLEQNQVYGITIISGLPPE-KPKN-----LSCIVNEGKQKRCWDG 148

Qy  123 GRNTPSDTNYTL-YYWHSLEKIHQCNIFREGQYFGCSFDLTKVKDSSFQHSVQIMVK 181
Db  149 GRETHLETNFTLKSEW--ATHKPADCK--AKRDTPTCTVDYSTV---YFVNIEVWVEAE 201

Qy  182 DNAGKI-KPSFNIVPLTSRVKPPPHIKNLSFHND-----LYVQWENPQNFISRCLEFYE 235
Db  202 NALGKVTSDHINFDPV-YKVKPNPPH--NLSVINSEELSLKLTWTNPSIKSVIILKYN 258

Qy  236 VEVNNSQTETHNVFVQEAECENPEFENVENTSCENVPGVLPDPLNTVIRVKTNKLKY 295
Db  259 IQYRTKDASTWS-----QIPP-EDTASTRSSFTVQDLKPFTEVVRIR-----CM 302

Qy  296 EDD--KLWSNWSQBSMS 309
Db  303 KEDGKGYSWDSSEAS 318

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Search completed: February 8, 2006, 22:35:24
Job time : 7.97472 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 21:52:58 : Search time 123.412 Seconds
(without alignments)
1427.670 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426
Perfect score: 2172
Sequence: 1 APFETQPPVNLVSVENLC.....QTKETDSVVLIENLKASQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004as.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	414	8	ADP84617 Human bre
2	2172	100.0	426	2	ADP84616 Human bre
3	2172	100.0	427	2	ADQ65618 Novel hum
4	2172	100.0	427	4	AAR22212 Sequence
5	2172	100.0	427	8	AAR22211 Sequence
6	2172	100.0	427	8	AAR22217 Sequence
7	2172	100.0	427	8	ADZ58697 Mouse IL-
8	2172	100.0	427	8	ADZ58698 Human IL-
9	2172	100.0	427	8	ADZ58698 Human IL-
10	2166	99.7	427	8	ADZ58698 Human IL-
11	2165	99.7	427	7	ADL71813 Canine IL-
12	2165	99.7	427	8	ADL71814 Human int
13	2159	99.4	427	4	AAU69136 Canine in
14	1869	86.0	405	4	AAU69136 Canine in
15	1784.5	82.2	664	7	ADP17841 Canine IL-
16	1749.5	80.5	784	3	AAU69136 Canine in
17	1749.5	80.5	784	3	AAU69136 Canine in
18	1745	80.3	322	5	AAE13745 Human sol
19	1745	80.3	793	3	AAU69136 Canine in
20	1745	80.3	793	3	AAU69136 Canine in
21	1698	78.2	426	2	AAU69136 Canine in
22	1688.5	77.7	424	9	ADZ58698 Human int
23	1536	70.7	286	4	AAU69136 Canine in
24	942	43.4	177	2	AAU69136 Canine in

25	465	21.4	134	8	ADP84617	Human bre
26	463	21.3	172	8	ADP84616	Human bre
27	463	21.3	226	8	ADQ65618	Novel hum
28	318	14.6	398	2	AAR22212	Sequence
29	318	14.6	415	2	AAR22211	Sequence
30	318	14.6	415	2	AAR22217	Sequence
31	318	14.6	415	5	ADZ58697	Mouse IL-
32	310	14.3	365	4	AAU69136	Canine in
33	310	14.3	386	4	AAU69135	Canine in
34	304.5	14.0	561	4	AAU69138	Canine IL
35	303.5	14.0	561	4	AAU69141	Canine IL
36	302	13.9	372	2	AAW36616	Celebus m
37	297	13.7	565	4	AAU69139	Canine IL
38	296.5	13.7	420	5	ADZ58698	Human IL-
39	296.5	13.7	421	2	AAR25064	Human IL-
40	296	13.6	318	4	AAU69137	Canine IL
41	296	13.6	563	4	AAU69140	Canine IL
42	294.5	13.6	380	2	AAW36613	Human Zcy
43	294.5	13.6	380	2	AAW35295	Human IL-
44	294.5	13.6	380	2	AAW24972	Human int
45	294.5	13.6	380	2	AAW33603	Homo sapi

ALIGNMENTS

RESULT 1
ADX97531
ID ADX97531 standard; protein; 414 AA.
XX AC ADX97531;
XX AC
DT 21-APR-2005 (first entry)
XX DE Pancreatic cancer associated human protein, SEQ ID 79.
XX KW pancreas tumor; cytostatic.
XX OS Homo sapiens.
XX FN EP1471075-A2.
XX PD 27-OCT-2004.
XX PF 31-MAR-2004; 2004EP-00090124.
XX PR 31-MAR-2003; 2003DE-01015834.
XX PA (HINZ/) HINZMANN B.
XX PA (ROSE/) ROSENTHAL A.
XX PA (PILA/) PILARSKY C.
XX PA (DAHL/) DAHL E.
XX PA (SPEC/) SPECHT T.
XX PA (LICHT/) LICHTNER R.
XX PI Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T;
XX PI Lichtner R, Staub E, Roepcke S, Li X;
XX WPI; 2004-768082/76.
XX N-PSDB; ADX97460.
XX PT New nucleic acid differentially expressed in pancreatic tumor tissue, for
XX use as diagnostic agents and in screening for therapeutic agents.
XX PS Claim 2; SEQ ID NO 79; 28pp; German.
XX CC The invention relates to a novel human nucleic acid sequence of the
XX CC pancreas and its encoded protein. The invention further comprises:
XX CC proteins and peptides, preferably isolated, that contain a sequence
XX CC encoded by the novel nucleic acid; and methods for diagnosis and
XX CC treatment of pancreatic cancer, using a substance that inhibits or binds
XX CC to the protein or its DNA, including: an antisense oligonucleotide, short
XX CC interfering RNA or ribozyme directed against the pancreatic protein, an

Db 266 SQTETHNVFVQEAKECPERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 325
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIIVPVI VAGAIIVLLVLLKRLKIIIFPPIDPGKIFK 360
Db 326 WSNWSQEMSGKGRNSTLYITMLLIIVPVI VAGAIIVLLVLLKRLKIIIFPPIDPGKIFK 385
Qy 361 EMFGDQNDTLLHWKXYDIYEKQTKETDSVVLIENLKKASQ 401
Db 386 EMFGDQNDTLLHWKXYDIYEKQTKETDSVVLIENLKKASQ 426

RESULT 3
AAW24973
ID AAW24973 standard; protein; 427 AA.
XX AC AAW24973;
XX DT 22-JUN-1998 (first entry)
XX DE Human interleukin-13 alpha receptor.
XX KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
XX OS Homo sapiens.
XX PN W09720926-A1.
XX PD 12-JUN-1997.
XX PF 07-NOV-1996; 96WO-FR001756.
XX PR 06-DEC-1995; 95FR-00014424.
XX PA (SNF1) SANOFI SA.
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX DR WPI; 1997-319773/29.
XX DR N-PSDB; AAT85827.
XX New purified human interleukin-13 receptors - and related nucleic acids,
PT useful for diagnosis and treatment of inflammation, allergy, etc.
PS Claim 8; Page 46-47; 83pp; French.
XX
XX This sequence represents interleukin-13 (IL-13) alpha receptor. The
CC invention relates to new purified peptides comprising 380 or 427 amino
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC affinity, but acquires high affinity when associated with the IL-4
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC diagnostic probes to identify aberrant synthesis or genetic anomalies
CC such as loss of heterozygosity and rearrangements, or chromosomal
CC anomalies. They are also used for production of recombinant IL-13R beta
CC and alpha which can be used as IL-13 antagonists, specifically to
CC regulate IL-13-induced responses for treatment of inflammation and
CC allergy. IL-13 receptors are also useful as antisense molecules for gene
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC immunoassays) to diagnose diseases associated with abnormal expression of
CC IL-13 receptors; when coupled to a toxin also for treatment of
CC overproduction of IL-13R. Cells that express IL-13R at the surface are
CC used to identify ligands and modulators of IL-13R
SQ Sequence 427 AA;

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e-201;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTPNPEGASSNCSLWYFSHFQDKQDKKIAPETRASI 60
Db 27 APTETQPPVNLVSVENLCTVIWTPNPEGASSNCSLWYFSHFQDKQDKKIAPETRASI 86

Qy 61 EVPLNERICLVQSGQSTNESEKPSILVEKCI SPPEGDPE SAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGQSTNESEKPSILVEKCI SPPEGDPE SAVTELCIWHNLSYMKCSW 146
Qy 121 LPOGNTSPDNTYLYWHRSLEKIHQCENTIFREGQYFGCSFDLTWKXDSFQHSVOIMV 180
Db 147 LPOGNTSPDNTYLYWHRSLEKIHQCENTIFREGQYFGCSFDLTWKXDSFQHSVOIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHNDLLYQWENPQNFI SRCLFYEVENVN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHNDLLYQWENPQNFI SRCLFYEVENVN 266
Qy 241 SQTETHNVFVQEAKECPERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 300
Db 267 SQTETHNVFVQEAKECPERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYEDDKL 326
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIIVPVI VAGAIIVLLVLLKRLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIIVPVI VAGAIIVLLVLLKRLKIIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLLHWKXYDIYEKQTKETDSVVLIENLKKASQ 401
Db 387 EMFGDQNDTLLHWKXYDIYEKQTKETDSVVLIENLKKASQ 427

RESULT 4
AAB19807
ID AAB19807 standard; protein; 427 AA.
XX AC AAB19807;
XX DT 05-MAR-2001 (first entry)
XX DE Human interleukin-13 receptor alpha-1.
XX KW Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
XX KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Sig_peptide
FT Domain 27..347
FT /label= Extracellular_domain
FT Protein 28..427
FT /label= Mature_protein
FT Peptide 327..331
FT /note= "WSXWS motif conserved in the type-I cytokine
FT receptor superfamily"
FT Domain 348..367
FT /label= Transmembrane_domain
FT Domain 368..427
FT /label= Cytoplasmic_domain
FT Binding-site 405..408
FT /note= "YXXQ motif, consensus for STAT binding"
XX US6143871-A.
XX 07-NOV-2000.
XX 12-NOV-1997; 97US-00969125.
XX 13-DEC-1996; 96GB-00025899.
XX (GAUC/) GAUCHAT J.
XX (BONN/) BONNEFOY J.
XX Gauchat J, Bonnefoy J;
XX WPI; 2001-006445/01.

```
DR N-PSDB; AAA88907.
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT eczema, asthma or AIDS.
XX
PS Claim 2; Fig 1A; 26pp; English.
XX
CC The present sequence is that of a protein capable of binding human
CC interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
CC of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
CC from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
CC polypeptide can be used to inhibit IL-13 or IL-4 induced IgE synthesis in
CC B cells, useful in the treatment of diseases in which IgE or Th2
CC differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
CC rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC them which have been shed from cells as a result of disease, e.g. cancer,
CC leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC syndrome and toxoplasmosis
XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 2172; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e-201;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFHFQDKQDKIAPETRRSI 60
DB 27 APTETOPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFHFQDKQDKIAPETRRSI 86
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146
QY 121 LPGRNTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 147 LPGRNTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLEFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLEFYEVEVNN 266
QY 241 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKL 300
DB 267 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKL 326
QY 301 WSNWSQEMSGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLRLKLIIPPPIDPGKIPK 360
DB 327 WSNWSQEMSGKKRNSTLYITMLLIVPVI VAGAIIVLLLYLRLKLIIPPPIDPGKIPK 386
QY 361 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKASQ 401
DB 387 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKASQ 427

RESULT 5
ADL71812
XX ADL71812 standard; protein; 427 AA.
AC ADL71812;
DB
DT 20-MAY-2004 (first entry)
XX
DE Human interleukin-13 receptor alpha (IL-13 Ralpa) protein.
XX
KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX
XX Homo sapiens.
XX
```

```
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..427
FT /note= "Human mature IL-13 R protein"
FT Domain 27..347
FT /note = Extracellular domain
FT Domain 327..331
FT /note = WSXWS motif
FT Domain 368..427
FT /note = Cytoplasmic domain
PN US2004043921-A1.
PD 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX N-PSDB; ADL71811.
XX
PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
PS Claim 1; SEQ ID NO 9; 27pp; English.
XX
CC The invention relates to polypeptides capable of binding human
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpa. The
CC invention also relates to a method of treatment of a disease in which
CC IL13 and IL4 cause adverse effects. The method is useful for treating a
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
CC of the invention are useful in raising antibodies. It is also useful in
CC gene therapy. The present sequence is human interleukin-13 receptor alpha
CC (IL-13 Ralpa) protein.
XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 2172; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e-201;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFHFQDKQDKIAPETRRSI 60
DB 27 APTETOPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFHFQDKQDKIAPETRRSI 86
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146
QY 121 LPGRNTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 147 LPGRNTSPDNTYLYWHRSLKIHQCEINIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLEFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYQWENPQNFISRCLEFYEVEVNN 266
QY 241 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKL 300
DB 267 SQTETHNVFVYQAEKACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKL 326
XX
```

Qy	301	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	360
Db	327	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	386
Qy	361	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	401
Db	387	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	427
RESULT 6			
ADL82843	ADL82843 standard; protein; 427 AA.		
XX	AC	ADL82843;	
XX	DT	17-JUN-2004 (first entry)	
XX	DE	Human PRO2537, SEQ ID 45.	
XX	XX	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;	
KW	KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;	
KW	KW	Gene Therapy; PRO; B cell related disorder; cancer;	
KW	KW	immune-mediated inflammatory disease; human.	
XX	OS	Homo sapiens.	
XX	XX	WO2004024097-A2.	
XX	XX	25-MAR-2004.	
XX	XX	15-SEP-2003; 2003WO-US029097.	
XX	XX	16-SEP-2002; 2002US-0411392P.	
XX	XX	(GETH) GENENTECH INC.	
XX	XX	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;	
PI	PI	Wu TD;	
XX	XX	WPI; 2004-329389/30.	
DR	DR	N-PSDB; ADL82842.	
XX	XX	New PRO polypeptide, useful for diagnosing and treating a B cell related	
PT	PT	disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune	
PT	PT	mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.	
XX	XX	Claim 10; Fig 45; 695pp; English.	
XX	XX	The present invention relates to PRO proteins and their coding sequences.	
CC	CC	The PRO proteins are useful for diagnosing and treating a B cell related	
CC	CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide	
CC	CC	antigen unresponsiveness, selective IgA deficiency, selective IgM	
CC	CC	deficiency, selective deficiency of IgG subclasses, immunodeficiency with	
CC	CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's	
CC	CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II	
CC	CC	hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic	
CC	CC	anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or	
CC	CC	ankylosing spondylitis. The PRO proteins are also useful for preparing a	
CC	CC	medicament for treating a condition that is responsive to the PRO	
CC	CC	protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO	
CC	CC	coding sequences are useful as hybridization probes in chromosome and	
CC	CC	gene mapping, in preparing PRO proteins, or in generating transgenic	
CC	CC	animals or knockout animals, which in turn are useful in the development	
CC	CC	and screening of therapeutically useful reagents.	
XX	XX	Sequence 427 AA;	
Qy	Query Match		
XX	Best Local Similarity 100.0%; Score 2172; DB 8; Length 427;		
XX	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 APTEQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI		
XX	60		

Db	27	APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI	86
Qy	61	EVLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW	120
Db	87	EVLNERICLQVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW	146
Qy	121	LPGRNTSPDNTYTLYYWHRSLKIHQCENTIFREGQYFGCSFDLTWKVDSFSEQHSVQIMV	180
Db	147	LPGRNTSPDNTYTLYYWHRSLKIHQCENTIFREGQYFGCSFDLTWKVDSFSEQHSVQIMV	206
Qy	181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVENVN	240
Db	207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVENVN	266
Qy	241	SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDLTNTVIRVTKNKLCEYEDDKL	300
Db	267	SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDLTNTVIRVTKNKLCEYEDDKL	326
Qy	301	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	360
Db	327	WSNWSQMSIGKKNSTLYITMLLIVPVIVAGAIIVLLVLRKLIIFPPIDPGKIFK	386
Qy	361	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	401
Db	387	EMFGDQNDTLHWKKYDIYEKQTKETDSVVLLENLAKASQ	427
RESULT 7			
ADN04504	ADN04504 standard; protein; 427 AA.		
XX	AC	ADN04504;	
XX	DT	01-JUL-2004 (first entry)	
XX	DE	Antipsoriatic protein sequence #445.	
XX	XX	antipsoriatic; gene therapy; psoriasis; diagnosis.	
XX	OS	Homo sapiens.	
XX	XX	WO2004028479-A2.	
XX	XX	08-APR-2004.	
XX	XX	25-SEP-2003; 2003WO-US030907.	
XX	XX	25-SEP-2002; 2002US-0414006P.	
XX	XX	(GETH) GENENTECH INC.	
XX	XX	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;	
PI	PI	Wu TD;	
XX	XX	WPI; 2004-305105/28.	
DR	DR	N-PSDB; ADN04503.	
XX	XX	New PRO nucleic acid or polypeptide, useful for preparing a	
PT	PT	pharmaceutical composition for diagnosing or treating psoriasis in a	
PT	PT	mammal.	
XX	XX	Claim 9; SEQ ID NO 898; 3069pp; English.	
XX	XX	The invention relates to novel polynucleotide and polypeptides for	
CC	CC	treating psoriasis or a sequence having at least 80% identity to the	
CC	CC	above sequences. The nucleic acid is useful for preparing a composition	
CC	CC	for diagnosing or treating psoriasis in a mammal. This sequence	
CC	CC	corresponds to one of the polypeptides of the invention.	
XX	XX	Sequence 427 AA;	
Qy	Query Match		
XX	Best Local Similarity 100.0%; Score 2172; DB 8; Length 427;		
XX	Matches 401; Conservative 100.0%; Pred. No. 3.3e-201;		

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 60
Db	
QY	27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWTFSHFGDKQDKKIAPETRRSI 86
Db	
QY	61 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db	
QY	87 EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Db	
QY	121 LPGRNTSPDNTYLYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 180
Db	
QY	147 LPGRNTSPDNTYLYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV 206
Db	
QY	181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQVQWENPQNFISRCLFYFEVNN 240
Db	
QY	207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQVQWENPQNFISRCLFYFEVNN 266
Db	
QY	241 SQTETHNVFYQSAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNKLCYEDDKL 300
Db	
QY	267 SQTETHNVFYQSAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNKLCYEDDKL 326
Db	
QY	301 WSNWSQEMSIGKKRNTLYITMLLIVPVIVAGAIIVLLLYLKRKLIIPFPDPGKIFK 360
Db	
QY	327 WSNWSQEMSIGKKRNTLYITMLLIVPVIVAGAIIVLLLYLKRKLIIPFPDPGKIFK 386
Db	
QY	361 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 401
Db	
QY	387 EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427
Db	
RESULT 8	
ADN62575	
ID	ADN62575 standard; protein; 427 AA.
XX	AC ADN62575;
XX	AC ADN62575;
DT	12-AUG-2004 (first entry)
XX	DE Human interleukin 13 (IL-13) receptor alpha 1 chain.
XX	XX Human; receptor; cytokine; interleukin 13 receptor alpha 1 chain; IL-13;
XX	XX IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX	XX cancer; inflammatory disease; rheumatoid arthritis;
XX	XX inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;
XX	XX lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis;
XX	XX urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;
XX	XX Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;
XX	XX Lyme disease; tuberculosis; malaria; leishmaniasis.
OS	Homo sapiens.
XX	XX
XX	XX
XX	XX
FT	Key Location/Qualifiers
FT	Peptide 1..26 "Signal peptide"
FT	/notes= "Signal peptide"
FT	27..427
FT	/notes= "Mature protein claimed in claim 1"
XX	US6743604-B1.
XX	PN
XX	XX
PD	01-JUN-2004.
XX	XX
XX	06-APR-2000; 2000US-00545002.
XX	XX
XX	13-DEC-1996; 96GB-00025899.
PR	PR 12-NOV-1997; 97US-00969125.
XX	XX
XX	(SMIK) SMITHKLINE BEECHAM CORP.
PA	Bonnefoy J, Gauchat J;
PI	WPI; 2004-409324/38.
XX	XX
DR	N-PSDB; ADN62574.
XX	XX

XX	New isolated nucleic acid molecule encoding a polypeptide capable of binding human IL-13 and/or binding human IL-4, useful in medicine, in diagnostics or for producing antibodies.	
PT	Claim 1; SEQ ID NO 9; 24pp; English.	
PS	The invention relates to an isolated nucleic acid molecule (ADN62574), which encodes the mature form of a polypeptide capable of binding human IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are a vector comprising the nucleic acid molecule and a host cell comprising the vector. The nucleic acids are useful as probes or primers or in the analysis of allelic variation. The polypeptides are useful for binding human IL-13 and/or binding human IL-4 and act as inhibitors by interfering with the interaction between human IL-13 or IL-4 and their natural receptors. They can also be used in medicine, e.g. for treatment of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy, Lyme disease, tuberculosis, malaria and leishmaniasis). They can also be used for producing antibodies, which can be used for diagnosing diseases. The present sequence represents IL-13 receptor alpha 1 subunit.	
XX	Sequence 427 AA;	
QY	Query Match 100.0%; Score 2172; DB 8; Length 427;	
Db	Best Local Similarity 100.0%; Pred. No. 3.3e-201;	
QY	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1	APTE	60
27	APTE	86
61	EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW	120
87	EVPLNERICLVGSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW	146
121	LPGRNTSPDNTYLYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV	180
147	LPGRNTSPDNTYLYWHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSEFEQHSVQIMV	206
181	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQVQWENPQNFISRCLFYFEVNN	240
207	KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFNHDDLQVQWENPQNFISRCLFYFEVNN	266
241	SQTETHNVFYQSAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNKLCYEDDKL	300
267	SQTETHNVFYQSAKCNPEFERNVENTSCFMVPGVLPDTLNTVTRVTKNKLCYEDDKL	326
301	WSNWSQEMSIGKKRNTLYITMLLIVPVIVAGAIIVLLLYLKRKLIIPFPDPGKIFK	360
327	WSNWSQEMSIGKKRNTLYITMLLIVPVIVAGAIIVLLLYLKRKLIIPFPDPGKIFK	386
361	EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ	401
387	EMFGDQNDTLHWKKYDIYEKQTKETSDSVLIENLKASQ	427
RESULT 9		
ABM82441		
ID	ABM82441 standard; protein; 427 AA.	
XX	XX	
AC	ABM82441;	
XX	XX	
DT	18-NOV-2004 (first entry)	
XX	XX	
DE	Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.	
XX	XX	
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;	

tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
gene therapy; cytostatic.
Homo sapiens.
WO2004030615-A2.
15-APR-2004.
29-SEP-2003; 2003WO-US028547.
02-OCT-2002; 2002US-0414971P.
(GETH) GENENTECH INC.
Wu TD, Zhang Z, Zhou Y;
WPI; 2004-347921/32.
N-PSDB; ACN41073.
New tumor-associated antigenic target polypeptides and nucleic acids,
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
prostate cancer or tumor.
Claim 12; SEQ ID NO 6271; 7273pp; English.
The invention relates to human tumour-associated antigenic target (TAT)
polypeptides, and their related nucleic acids. The TAT polypeptides are
overexpressed in cancer tissues compared to normal tissues, and may thus
serve as effective targets for the diagnosis and treatment of cancer in
mammals. The invention also relates to nucleic acid and polypeptide
sequences at least 80% identical to the TAT nucleic acids and
polypeptides; expression vectors and host cells comprising a TAT nucleic
acid; an antibody specific for a TAT polypeptide; a peptide or organic
molecule which binds to a TAT polypeptide; fusion proteins comprising a
TAT polypeptide; and methods and compositions for the treatment or
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
antibodies, antagonists, binding molecules and compositions are useful
for diagnosing or treating a cell proliferative disorder associated with
increased TAT expression, particularly cancers such as breast cancer,
colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
cancer, pancreatic cancer, cervical cancer, cancers of the central
nervous system, melanoma and leukaemia. TAT nucleic acids may further be
used as hybridisation probes, in chromosome and gene mapping, in
chromosome identification and in gene therapy. The present sequence
represents a TAT polypeptide of the invention
SQ Sequence 427 AA;
Query Match 100.0%; Score 2172; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. NO. 3.3e-201;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APETQPPVNLVSVENLCTVIWNPPEGASSNSLWYFSGHFGDKQDKKIAPETRISI 60
DB 27 APETQPPVNLVSVENLCTVIWNPPEGASSNSLWYFSGHFGDKQDKKIAPETRISI 86
QY 61 EYPLNERICLQVGSQCSTNESEKPSILVEKCI SPPEGDPESA VTELQCIWHNLSYMKCSW 120
DB 87 EYPLNERICLQVGSQCSTNESEKPSILVEKCI SPPEGDPESA VTELQCIWHNLSYMKCSW 146
QY 121 LFGRTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLT VKVQDSSFEQHSVQIMV 180
DB 147 LFGRTSPDNTYLYYHRSLEKIHCENIFREGQYFGCSFDLT VKVQDSSFEQHSVQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKDDPHIKNLSHNDLLYVQWENPQNFISRCILFYEVVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKDDPHIKNLSHNDLLYVQWENPQNFISRCILFYEVVNN 266

QY 241 SQTEHNVFYVQBAKCNPFERNVENTSCFMVGVLPD TLNTRIRVKTNKL CYEDDKL 300
DB 267 SQTEHNVFYVQBAKCNPFERNVENTSCFMVGVLPD TLNTRIRVKTNKL CYEDDKL 326
QY 301 WSNWSQMSIGKKNSTLYITMLLI VPIVAGAIIVLLLYLKRLLIIFPPDPGKIFK 360
DB 327 WSNWSQMSIGKKNSTLYITMLLI VPIVAGAIIVLLLYLKRLLIIFPPDPGKIFK 386
QY 361 EMFGDQNDTLHWKKYDIYERKQTEETDSVVLIENLKKASQ 401
DB 387 EMFGDQNDTLHWKKYDIYERKQTEETDSVVLIENLKKASQ 427
RESULT 10
ADL71813
ID ADL71813 standard; protein; 427 AA.
XX AC ADL71813;
XX DT 20-MAY-2004 (first entry)
XX DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, T1301.
XX KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
XX KW mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 130 /note= "Wild-type Thr is substituted with Ile"
XX PN US2004043921-A1.
XX PD 04-MAR-2004.
XX PF 29-SEP-2003; 2003US-00671697.
XX PR 13-DEC-1996; 96GB-00025899.
PR 12-NOV-1997; 97US-00969125.
XX PR 06-APR-2000; 2000US-00545002.
XX PA (BONN/) BONNEFOY J.
XX PI (GAUC/) GAUCHAT J.
XX PI Bonnefoy J, Gauchat J;
XX DR WPI; 2004-225726/21.
XX PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX PS Claim 14; Page; 27pp; English.
XX CC The invention relates to polypeptides capable of binding human
interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
invention also relates to a method of treatment of a disease in which
IL13 and IL4 cause adverse effects. The method is useful for treating a
disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
of the invention are useful in raising antibodies. It is also useful in
gene therapy. The present sequence is human interleukin-13 receptor alpha
(IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
CC specification, however it is constructed based on human IL-13 Ralpha
protein shown as SEQ ID NO:9 in the specification.
XX SQ Sequence 427 AA;
Query Match 99.7%; Score 2166; DB 8; Length 427;

Best Local Similarity 99.8%; Pred. No. 1.3e-200; Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTETQPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRI 60
 DB 27 APTETQPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRI 86
 QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 120
 DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 146
 QY 121 LPRGNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSVQIMV 180
 DB 147 LPRGNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSVQIMV 206
 QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLEFVEVNN 240
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLEFVEVNN 266
 QY 241 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKL CYEDDKL 300
 DB 267 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKL CYEDDKL 326
 QY 301 WSNWSQEMSGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
 DB 327 WSNWSQEMSGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 386
 QY 361 EMFGDQNDTLLHWKDYDIYEKOTKEETDSVVLJENLKASQ 401
 DB 387 EMFGDQNDTLLHWKDYDIYEKOTKEETDSVVLJENLKASQ 427

RESULT 11 ;
 ADL17835
 ID ADL17835 standard; protein; 427 AA.
 AC ADL17835;
 XX
 XX 12-FEB-2004 (first entry)
 DT Human IL-13 alpha 1 receptor (IL-13R) protein.
 DE IL-13R; human; receptor; anaphylaxis; hay fever; asthma;
 KW antiinflammatory; cytostatic; antiulcer; dermatological; antiallergic;
 KW antiasthmatic; fibrosis; Hodgkin's disease; ulcerative colitis;
 KW scleroderma; allergic rhinitis; oncological;
 KW chronic obstructive pulmonary disease.
 XX Homo sapiens.
 OS
 XX WO2003080675-A2.
 FN
 XX 02-OCT-2003.
 PD
 XX 21-MAR-2003; 2003WO-AU000352.
 PF
 XX 22-MAR-2002; 2002AU-00001301.
 PR
 PR 03-FEB-2003; 2003AU-00900437.
 XX
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA
 XX Dunlop FM, Baca M, Nash AD, Fabri LJ;
 PI WPI; 2003-876912/81.
 XX DR N-PSDB; ADF17834.
 DR
 XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
 PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
 FT scleroderma, allergic rhinitis, oncological conditions, asthma or an
 PT inflammatory disorder.
 XX
 XX Disclosure; SEQ ID NO 4; 99pp; English.

CC This invention relates to a novel antibodies that function as interleukin
 CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
 CC for treating certain conditions induced by IL-13. Specifically, it refers
 CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
 CC and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
 CC system, such that it is involved in the induction of IGE, IgG4 and T-
 CC helper cells and accordingly is implicated in conditions from anaphylaxis
 CC to hay fever and asthma. As such, the present invention describes these
 CC novel antibodies as antiinflammatory, cytostatic, antiulcer,
 CC dermatological, antiallergic and antiasthmatic. The methods and
 CC compositions are useful for treating various disorders including
 CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
 CC rhinitis, oncological conditions and chronic obstructive pulmonary
 CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor
 CC protein of the invention.
 XX
 SQ Sequence 427 AA;

Query Match 99.7%; Score 2165; DB 7; Length 427;
 Best Local Similarity 99.8%; Pred. No. 1.6e-200; Mismatches 1; Indels 0; Gaps 0;
 Matches 400; Conservative 0;

QY 1 APTETQPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRI 60
 DB 27 APTETQPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRRI 86
 QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 120
 DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKCI SPPEGDPESAVTELOCIWHNLSYMKCSW 146
 QY 121 LPRGNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSVQIMV 180
 DB 147 LPRGNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFEGHSVQIMV 206
 QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLEFVEVNN 240
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLEFVEVNN 266
 QY 241 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKL CYEDDKL 300
 DB 267 SQTETHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVTRIRVTKNKL CYEDDKL 326
 QY 301 WSNWSQEMSGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 360
 DB 327 WSNWSQEMSGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIDPGKIFK 386
 QY 361 EMFGDQNDTLLHWKDYDIYEKOTKEETDSVVLJENLKASQ 401
 DB 387 EMFGDQNDTLLHWKDYDIYEKOTKEETDSVVLJENLKASQ 427

RESULT 12
 ADL71814
 ID ADL71814 standard; protein; 427 AA.
 XX
 AC ADL71814;
 XX
 XX 20-MAY-2004 (first entry)
 DT Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.
 DE
 XX Human, IL-13; IL-4; IL-4 R; atopy; atopie dermatitis; allergy; rhinitis;
 KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
 KW mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 358
 FT /note= "Wild-type Gly is substituted with Asp"
 XX
 XX US2004043921-A1.

XX 04-MAR-2004.
XX 29-SEP-2003; 2003US-00671697.
XX 13-DEC-1996; 96GB-00025899.
XX 12-NOV-1997; 97US-00969125.
XX 06-APR-2000; 2000US-00545002.
XX (BONN/) BONNEFOY J.
XX (GAUC/) GAUCHAT J.
XX Bonnefoy J, Gauchat J;
XX WPI; 2004-225726/21.
XX
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX Claim 14; Page; 27pp; English.
XX
XX The invention relates to polypeptides capable of binding human
XX interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX invention also relates to a method of treatment of a disease in which
XX IL13 and IL4 cause adverse effects. The method is useful for treating a
XX disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX of the invention are useful in raising antibodies. It is also useful in
XX gene therapy. The present sequence is human interleukin-13 receptor alpha
XX (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the
XX specification, however it is constructed based on human IL-13 Ralpha
XX protein shown as SEQ ID NO:9 in the specification.
XX
XX Sequence 427 AA;
XX
XX Query Match 99.7%; Score 2165; DB 8; Length 427;
XX Best Local Similarity 99.8%; Pred. No. 1.6e-200; Indels 0; Gaps 0;
XX Matches 400; Conservative 0; Mismatches 1;
XX
XX 1 APTQTQPTVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKQDKKIAPETRRI 60
XX 27 APTQTQPTVNLVSVENLCTVIWTWNPPEGASSNCSLWYFHFSGDKQDKKIAPETRRI 86
XX
XX 61 EVPLNERICLVGSCQSTNBESEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW 120
XX 87 EVPLNERICLVGSCQSTNBESEKPSILVEKICISPPGDPESAVTELCIWNLSYMKCSW 146
XX
XX 121 LPRGNTSPDNTYLLYHRSLEKIHOCENIPREGQYFGCSFDLTGVKQSSFEQHSVQIMV 180
XX 147 LPRGNTSPDNTYLLYHRSLEKIHOCENIPREGQYFGCSFDLTGVKQSSFEQHSVQIMV 206
XX
XX 181 KDNAGKIPSFNIVPLTSRVKPDPPHKNLSFHNDDLVQVENPQNFISRCILFVEVYNN 240
XX 207 KDNAGKIPSFNIVPLTSRVKPDPPHKNLSFHNDDLVQVENPQNFISRCILFVEVYNN 266
XX
XX 241 SQTETHNVFYVQKACNPEPERNVNVENTSCFMPVGVLPDNLTVIRVKTNKLCEYDDKL 300
XX 267 SQTETHNVFYVQKACNPEPERNVNVENTSCFMPVGVLPDNLTVIRVKTNKLCEYDDKL 326
XX
XX 301 WSNWQSEMSIGKRRNSTLYITMLLVIPVIVAGAILVLLYLKRLKLIIPFPDPGKIFK 360
XX 327 WSNWQSEMSIGKRRNSTLYITMLLVIPVIVADAIIVLLYLKRLKLIIPFPDPGKIFK 386
XX
XX 361 EMFGQNDTLLHWKYDYIEKQTKETDSVLIENLKKASQ 401
XX 387 EMFGQNDTLLHWKYDYIEKQTKETDSVLIENLKKASQ 427

AC AAB19808;
XX 05-MAR-2001 (first entry)
XX Human interleukin-13 receptor alpha-1 variant.
XX
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
XX atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= sig_peptide
XX Domain 27..347
XX /label= Extracellular_domain
XX Protein 28..427
XX /label= Mature_protein
XX Misc-difference 130
XX /note= "Gly in "
XX Peptide 327..331
XX /note= "NSXWS motif conserved in the type-I cytokine
XX receptor superfamily"
XX Domain 348..367
XX /label= Transmembrane_domain
XX Domain 368..427
XX /label= Cytoplasmic_domain
XX Binding-site 405..408
XX /note= "YXXQ motif, consensus for STAT binding"
XX
XX US6143871-A.
XX
XX 07-NOV-2000.
XX
XX 12-NOV-1997; 97US-00969125.
XX
XX 13-DEC-1996; 96GB-00025899.
XX (GAUC/) GAUCHAT J.
XX (BONN/) BONNEFOY J.
XX Gauchat J, Bonnefoy J;
XX WPI; 2001-006445/01.
XX
XX Novel polypeptide capable of binding interleukin-13 or interleukin-4
XX useful for treating atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma or AIDS.
XX
XX Claim 4; -: 26pp; English.
XX
XX The present sequence is that of a claimed isolated polypeptide which is
XX capable of binding human interleukin-13 (IL-13) and/or human interleukin-
XX 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a
XX sequence (see AAB19807) deduced from isolated cDNA by having residue 130
XX as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13
XX receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4
XX induced IgE synthesis in B cells, useful in the treatment of diseases in
XX which IgE or Th2 differentiation plays a role, e.g. atopy, atopic
XX dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised
XX against the polypeptide are useful for detecting IL-13 and IL-4 receptor
XX or parts of them which have been shed from cells as a result of disease,
XX e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma, lupus erythematosus, AIDS, thyroditis, diabetes,
XX uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
XX inflammatory bowel disease, glomerulonephritis, ulcerative colitis,
XX Crohn's disease, Sjogren's syndrome and toxoplasmosis. Note: The present
XX sequence is not shown in the specification but is derived from the IL-13
XX receptor alpha 1 sequence given in figure 1 (see AAB19807)
XX
XX Sequence 427 AA;


```
Query Match      99.4%; Score 2159; DB 4; Length 427;
Best Local Similarity 99.5%; Pred. No. 6.1e-200; Mismatches 2; Indels 0; Gaps 0;
Matches 399; Conservative 0;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRISI 60
DB 27 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRISI 86

QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 87 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146

QY 121 LPGNTSPDNTYLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 147 LPGNTSPDNTYLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206

QY 181 KDNAGKIKPSFNIVPLTSRVKPPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVEVNN 240
DB 207 KDNAGKIKPSFNIVPLTSRVKPPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVEVNN 266

QY 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYEDDKL 300
DB 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYEDDKL 326

QY 301 WSNWSQEMSIGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIPPPIDPGKIFK 360
DB 327 WSNWSQEMSIGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIPPPIDPGKIFK 386

QY 361 EMFGDQNDTLHWKYYDIYEKQTEEDTSVVLLENLKKASQ 401
DB 387 EMFGDQNDTLHWKYYDIYEKQTEEDTSVVLLENLKKASQ 427

RESULT 14
AAU69132
ID AAU69132 standard; protein; 405 AA.
AC AAU69132;
XX
XX
XX 29-JAN-2002 (first entry)
XX
XX Canine interleukin 13 receptor PcaIL-13Ralpha1 405.
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IGG FC;
XX immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
XX immune response.
XX
XX Canis familiaris.
XX
XX WO200177332-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011498.
XX
XX 07-APR-2000; 2000US-0195659P.
XX 07-APR-2000; 2000US-0195874P.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
XX
XX N-PSDB; AAS59954, AAS59956.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G protein
XX or canine interleukin-13 receptor protein useful for regulating immune
XX response of an animal and for developing regulatory compounds.
XX
XX Claim 18; Page 164-165; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
```

```
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor
CC protein, the nucleic acids encoding them, antibodies raised against them,
CC fusion proteins between the Igg and IL-13R proteins and methods of
CC isolating regulators of them. The regulators are useful for regulating an
CC immune response in a canine. The proteins useful to develop regulatory
CC compounds including inhibitors and activators that, when administered to
CC a canine in an effective manner, are capable of protecting canine from
CC disease mediated by IL-13Ralpha or IL-13. The regulators are useful for
CC treating canine Igg (heavy and/or light chain) and/or canine IL-13R
CC mediated responses. The molecules of the invention are useful to regulate
CC the immune response of an animal (e.g. by gene therapy). The present
CC sequence represents a protein of the invention
XX
SQ Sequence 405 AA;

Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 7.1e-172;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRISI 60
DB 5 APTETQPPVNLVSVENLCTVIWTWNPPEGASSNCSLWTFSHFGDKQDKKIAPETRISK 64

QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 65 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCTW 124

QY 121 LPGNTSPDNTYLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
DB 125 LPGNTSPDNTYLYYHRSLEKIHQENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 184

QY 181 KDNAGKIKPSFNIVPLTSRVKPPDPHINKLSFNHDDLIVQWENPQNFISRCCLFYEVEVNN 240
DB 185 KDNARKIRPSFNIVPLTSRVKPPDPHINKLFFQGNLYVQMKNPQNFYSRCLSYQVEVNN 244

QY 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYEDDKL 300
DB 245 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDTLNTRIRVKTNKLCEYEDDKL 304

QY 301 WSNWSQEMSIGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIPPPIDPGKIFK 360
DB 305 WSNWSQAMSGENTDPTFYITMLLATQVIVAGAIIVLLLYLKLKIIIPPPIDPGKIFK 364

QY 361 EMFGDQNDTLHWKYYDIYEKQTEEDTSVVLLENLKKASQ 401
DB 365 EMFGDQNDTLHWKYYDIYEKQTEEDTSVVLLENLKKASQ 405

RESULT 15
ADF17841
ID ADF17841 standard; protein; 664 AA.
XX
XX ADF17841;
XX
XX 12-FEB-2004 (first entry)
XX
XX Chimeric human IL-13R alpha 1-gp130 fusion protein.
XX
XX IL-13R alpha 1-gp130; human; receptor; chimeric; anaphylaxis; hay fever;
XX asthma; antiinflammatory; cytostatic; antiulcer; dermatological;
XX antiallergic; antiasthmatic; fibrosis; Hodgkin's disease;
XX ulcerative colitis; scleroderma; allergic rhinitis; oncological;
XX chronic obstructive pulmonary disease.
XX
XX Chimeric.
XX
XX Homo sapiens.
XX
XX WO2003080675-A2.
XX
XX 02-OCT-2003.
XX
XX 21-MAR-2003; 2003WO-AU000352.
XX
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PR 22-MAR-2002; 2002AU-00001301.
PR 03-FEB-2003; 2003AU-00900437.
XX
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Dunlop FM, Baca M, Nash AD, Fabri LJ;
XX
XX WPI; 2003-876912/81.
XX N-ESDB; ADF17840.
XX
XX New monoclonal antibodies against interleukin-13 receptor alpha, useful
PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an
PT inflammatory disorder.
XX
XX Disclosure; SEQ ID NO 10; 99pp; English.
XX
XX This invention relates to a novel antibodies that function as interleukin
CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used
CC for treating certain conditions induced by IL-13. Specifically, it refers
CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13
CC and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory
CC system, such that it is involved in the induction of IgE, 1964 and T-
CC helper cells and accordingly is implicated in conditions from anaphylaxis
CC to hay fever and asthma. As such, the present invention describes these
CC novel antibodies as antiinflammatory, cytostatic, antiulcer,
CC dermatological, anti allergic and antiasthmatic. The methods and
CC compositions are useful for treating various disorders including
CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic
CC rhinitis, oncological conditions and chronic obstructive pulmonary
CC disease. This polypeptide sequence is the chimeric human IL-13R alpha 1-
CC gp130 fusion protein of the invention.
XX
XX Sequence 664 AA;
Query Match : 82.2%; Score 1784.5; DB 7; Length 664;
Best Local Similarity 91.7%; Pred. No. 2.3e-163;
Matches 333; Conservative 8; Mismatches 15; Indels 7; Gaps 3;
QY 1 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDGKQKKIAPETRISI 60
DB 45 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDGKQKKIAPETRISI 104
QY 61 EYPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCSW 120
DB 105 EYPLNERICLVGSCSTNESEKPSILVEKICISPEGDPESAVTELCIWHNLSYMKCSW 164
QY 121 LFGRTSPDNTYLYYWHRSLEKIHQCENIFREGQYFGCSFDLTWKDSSFEQHSVQIMV 180
DB 165 LFGRTSPDNTYLYYWHRSLEKIHQCENIFREGQYFGCSFDLTWKDSSFEQHSVQIMV 224
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPNQFISRCIFYEVEVNN 240
DB 225 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPNQFISRCIFYEVEVNN 284
QY 241 SQTETHNVFYQEAKECENPEPERNVENTSCFVWPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
DB 285 SQTETHNVFYQEAKECENPEPERNVENTSCFVWPGVLPDTLNTVIRVKTNKLCEYEDDKL 344
QY 301 WSNWSQEMSIGKRNSTLYITMLIIVPVIVAGAIL---VLLLYLKR--LKIIIPPIPD 354
DB 345 WSNWSQEMSIGKRNSTGEIB-AIVVPVCLAFLLTLLGLVLCFKNKRDLIKHHIWNVPD 403
QY 355 PGK 357
DB 404 PSK 406

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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:59:28 ; Search time 23.7733 Seconds
(without alignments)
1622.950 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426
Perfect score: 2172
Sequence: 1 APETQPPVTNLSVENVLC.....QTKKETDSVVLINLKASQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1649.5	75.9	426	2 JC7773	IL-13ralpha 1 prot
2	318	14.6	415	2 S12357	interleukin-5 rece
3	294.5	13.6	420	2 S21052	interleukin-5 rece
4	269.5	12.4	348	2 JC7907	common cytokine re
5	229	10.5	335	2 A40267	interleukin-5 rece
6	228	10.5	400	2 S06945	granulocyte-macrop
7	207	9.5	373	2 A55718	interleukin-2 rece
8	205.5	9.5	369	2 I49280	interleukin-2 rece
9	202	9.3	369	2 A42565	interleukin-2 rece
10	197.5	9.1	831	2 J01655	prolactin receptor
11	190	8.7	610	2 A34631	lactogen receptor
12	189	8.7	310	2 A29884	prolactin receptor
13	189	8.7	412	2 A41070	prolactin receptor
14	189	8.7	610	2 A36116	prolactin receptor
15	186	8.6	581	2 I45971	prolactin receptor
16	185	8.5	616	2 A30304	prolactin receptor
17	183	8.4	292	2 I7525	prolactin receptor
18	180	8.3	303	2 I77524	prolactin receptor
19	180	8.3	608	2 I53269	prolactin receptor
20	176	8.1	630	2 I51086	prolactin receptor
21	173	8.0	918	2 B36337	membrane glycoprot
22	172.5	7.9	288	2 A59405	prolactin receptor
23	172.5	7.9	376	2 A59405	prolactin receptor
24	172.5	7.9	622	2 A40144	prolactin receptor
25	170	7.8	897	1 A39255	cytokine receptor
26	165	7.6	396	2 S22909	interleukin-3 rece
27	163	7.5	830	2 I50455	prolactin receptor
28	162.5	7.5	333	2 S13684	granulocyte-macrop
29	161.5	7.4	1092	2 JX0312	differentiation-st

interleukin-3 rece
cytokine receptor
granulocyte-macrop
interleukin-3 rece
interleukin-3 rece
somatotropin recep
somatotropin recep
leukemia inhibitor
glycoprotein 130 -
interleukin-6 sign
somatotropin recep
somatotropin recep
erythropoietin rec
granulocyte-macrop
interferon alpha/b

ALIGNMENTS

RESULT 1

JC7773
IL-13ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7773
R:Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIR>
A:Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell proliferation

C:Genetics:

A:Gene: il-13ralpha

Query Match 75.9%; Score 1649.5; DB 2; Length 426;
Best Local Similarity 75.8%; Pred. No. 1.le-122; Indels 3; Gaps 2;
Matches 303; Conservative 43; Mismatches 51;

Qy 3 TETQPPVTNLSVENVLCIWTWNPPGASNCSLMYFSHFQDKQDKKIAPETRRSIEV 62
Db 27 TEVQPPVTNLSVENVLCIWTWSPGASPCSLRYFSHFDDQDDKKIAPETRRKKEL 86
Qy 63 PLNERICLVGSGQSTNESEKPSILVEKCISSPPGDPESAATELOCIWHNLSYMKCSWLP 122
Db 87 PLNEKICLVGSGQSTNESEKPSPLVKKICISPPRRGSESAVTELCQCTWHNLSYMKCSWLP 146
Qy 123 GRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTVKYKSSFEQHSVOIMVKD 182
Db 147 GKNTSPDNTYLYYSSLGSLQCENIHGHCISFKLTKV-ESNYEHNNIQLIMVKD 205
Qy 183 NAGKIKSENIPTLSRVKPPPHIKNLSFNDDLYVQWENPQNFISCLFYEVEVNSQ 242
Db 206 NAGKIRSPYKLVSTSNVKPPPHIKHFLKNGALFVQWKPNQNFSSRCLSEVEVNSTQ 265
Qy 243 TETH--NVFYVQEAECENPEFERNVENTSCFMPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 266 TDSYNSNLSVEEDKQCNSEFDRNNEGASCFISGVLXNTVTVVAVRVKTNKLCFDDNDL 325
Qy 301 WSNQWQMSIGCKRNSLYITMLLIVPVVAGAIIVLLYLKRLKLIIFPPPIPDGKIFPK 360
Db 326 WSNWSEALSIKGPNSFTYITMLLIIPVFVAIVIIILLFYLRKLIIFPPPIPDGKIFPK 385
Qy 361 EMFGQNDTTLHWKDYIEKQTKBEETDSVVLINLKAS 400
Db 386 EMFGQNDTTLHWKDYIEKQTKBEETDSVVLINLKAA 425

RESULT 2

S12357
interleukin-5 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12357
R;Takaki, S.; Tominaga, A.; Hitooshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takateu, K.
EMBO J. 9, 4367-4374, 1990
A;Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A;Reference number: S12357; MUID:91092260; PMID:2265612
A;Accession: S12357
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-415 <TAK>
A;Cross-references: UNIPROT:P21183; UNIPARC:UPI0000028472; GB:D90205; NID:g220465; PIDN:
C;Keywords: cytokine receptor; transmembrane protein

Query Match 14.6%; Score 318; DB 2; Length 415;
Best Local Similarity 23.9%; Pred. No. 1.9e-17;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 7 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYSHF-GDKQDKKIAPETRRSIEVPL 64
Db 29 PPV-NFTIKATGLAQVLLHWDPNPDQQRHVLDLEYHVKINAPQDEYDTRKTESKCVTPL 87
Qy 65 NERICLQVGSQCSTNESEKPSILVEKCSIPPEGDPESAVTELCIWHNL----- 113
Db 88 HEGFAASVRLTKSSHTTLASSWSWSELKAPPGSGTGVNLTCTTHTVVSSHTHLRPYQ 147
Qy 114 SYMKCSWLPGRNTSPDNTYLYWHRSLEKIHQCENIFRE--QGYFGCSPLDTKVKDSSF 171
Db 148 VSLRCTLWLGKADPEDTQYFLYRYFGVLTB--KQGEYSDALNRNTACWPPRTFINSKGF 205
Qy 172 EQHSVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHPIKNLSLPHNDLLYQWENPQN-FISR 230
Db 206 EQLAVHINGSKRAAIKPPDLQSPDLAIDQVNPFRNVTVIEISNLSYIQWEKPLSAFPDH 265
Qy 231 CLFEVEVNNSTQETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDNLNTRVRVKT 290
Db 266 CFNTELUKYNKNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAAV 309
Qy 291 NKLCEYDDKLSWNSQEMSGIKKRNSTLYITMLLIVPVIIVAGAIIVLLLYLKLKII--- 347
Db 310 SSPCPMPGR-WGWSQPIYVGKERKS-LVEMHLIVLP--TAACFVLLIFSLICRVCHLW 364
Qy 348 --IFPPIDPDKGIFKEMFGQNDOTLHWKKYDIYVKQTEETDSVV 391
Db 365 TRLFPVPVAPKSNIKDL-----PVTVEYKPSNETKIEV 399

RESULT 3
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored in
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S21052; S21050; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takateu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815; PMID:1732409
A;Accession: S21052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: UNIPROT:Q14633; UNIPARC:UPI000000729EE; EMBL:X61176; NID:g33843; PIDN:
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395, 'I', <MU2>
A;Cross-references: UNIPARC:UPI0000179A7F; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332, 'K', <MU3>
A;Cross-references: UNIPARC:UPI0000179A80; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:

A;Experimental source: clone lambda h5R.25
R;Tavernier, J.; Tupyens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
C;Accession: S12357
A;Reference number: A46175; MUID:92357767; PMID:1495999
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Cross-references: UNIPARC:UPI0000179A81
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128, 'I', 130-395, 'I', <MUW>
A;Cross-references: UNIPARC:UPI000006EDIC; EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128, 'I', 130-332, 'K', <MU4>
A;Cross-references: UNIPARC:UPI000006D11E; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
P;345-365/Domain: transmembrane #status predicted <TM>
P;35, 131, 137, 142, 216, 244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.6%; Score 294.5; DB 2; Length 420;
Best Local Similarity 24.8%; Pred. No. 1.4e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

Qy 7 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYSHFGDKQDKKIAPETRRSIEVPLN 65
Db 32 PPV-NFTIKVTGLAQVLLQWKPNDQEQRNVLLEY-----QVKINAPK-EDDYETRI 82
Qy 66 ERICLQV-----GSQCSTNESEKPSILVEKCS-----PPEGDPESAVTELCIWHNL--- 113
Db 83 ESKCVTLHKGFSAVSRTILQNDHSLASSWASAEHLHAPGSGTGVNLTCTTNTTEDN 142
Qy 114 -----SY-----MKCSWLPGRNTSPDNTYLYWHRSLEKIHQCENIFRE--QGYFGCSFDL 163
Db 143 YSLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGWSWTE--ECOYSKDTLGRNIACWFR 200
Qy 164 TKVKDSSPQHSVQIMVKNAGKIKPSFNIVPLTSRVKDPDPHPIKNLSLPHNDLLYQWEN 223
Db 201 TFLSKGRDMLAVLVNNGSSKHSAIRPDQQLFALHLDQINPLNLTABEGTSLSQWEK 260
Qy 224 PQN-FISRCFLFEVEVNNSTQETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDNLN 282
Db 261 PVSAPFIHCFDYEKIHNRNG-----YLQIEKLMTNFAISIIDLSKY----- 304
Qy 283 TVRIRVTKLKYEDDKLSWNSQEMSGIKKRNSTLYITMLLIVPVIIVAGAIIVLLLYLK 342
Db 305 DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLICK 363
Qy 343 --RLKIIIPPPIDPDKGIFKEMFGQNDOTLHWKKYDIYVKQTEETDSVVL 392
Db 364 ICHLWIKLFPPIAPKSNIKDLFVTTN-----YEKAGSSETEIEVI 404

RESULT 4
JC7907
common cytokine receptor gamma chain, isoform a - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7907
R;Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002

Qy	164	TKYKDSFEQHSVOIMVKONAGKIKPSFNIVPLTTSRVKDPDPHPIKXLSFHNDDLYQWEN	223	
		201	TFILSGROWLSVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEIGTRLISIQWEK	260
Db				
Qy	224	PQN-FTSRCLFYEVVNNSGTETHNVPYQSAKCENPEFERNVENTSCFVMPGVGLPDTLN	282	
Db	261	PVSAFP1HCPDYEVIKHTNRG-----YLQIEKLTMTNAPISIIDLSKY-----	304	
Qy	283	TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKR	314	
Db	305	DVQVRAAVSSMCREAG-LWSEWSOP1YVGFSR	335	

RESULT 6
S06945
granulocyte-macrophage colony-stimulating factor receptor A precursor - human
N;Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S06945; A41286; A44474
R;Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBO J. 8, 3667-3676, 1989
A;Title: Expression cloning of a receptor for human granulocyte-macrophage colony-
stimulating factor
A;Reference number: S06944; MUID: 90059966; PMID:2551171
A;Accession: S06945
A;Molecule type: mRNA
A;Residues: 1-400 <GPA>
A;Cross-references: UNIPROT:P15509; UNIPARC:UPI0000000C45; EMBL:X17648; NID:93222222
R;Crossler, K.E.; Wong, G.G.; Mathew-Prevot, B.; Nathan, D.G.; Steff, C.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
A;Title: A functional isoform of the human granulocyte/macrophage colony-stimul-
ating factor receptor
A;Reference number: A41286; MUID: 91352066; PMID:1715577
A;Accession: A41286
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 347-400 <CRO>
A;Cross-references: UNIPARC:UPI000017C141
R;Rappold, G.; Willson, T.A.; Henke, A.; Gough, N.M.
Genomics 14, 455-461, 1992
A;Title: Arrangement and localization of the human GM-CSF receptor alpha chain
A;Reference number: A44474; MUID: 93052350; PMID:1358805

A:Accession: **U01000**
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'M', 377-400 <RAP>
A:Cross-references: UNIPARC:UPI00000723FC; GB:S48539; NID:G258859; PIDN:AAB23394
A:Note: sequence extracted from NCBI backbone (NCBIP:117980)
C:Genetics:
A:Gene: GDB:CSF2RA; CSF2R
A:Cross-references: GDB:111877; OMIM:306250; OMIM:425000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-22/Domain: signal sequence status predicted <SIG>
F:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #8
F:322-346/Domain: transmembrane #status predicted <TM>
F:46:54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (CO
Onerv Match 10.5%; Score 228; DB 2; Length 400;

Query Match	10.5%	Score 228;	DB 2;	Length 400;
Best Local Similarity	22.4%	Pred. No. 2.4e-10;		
Matches	90;	Conservative	82;	Mismatches 180; Indels 50; Gaps 18
QY	5	TQPVTNLVSVENLCTVIWTNPPEGAS-SNCSLMWYSFHFGDKODKKIAPETRRSIEVP	63	
Db	29	TVAASSLNVRFDNR-TWLNSMDQCENTFSKFL-----TDKNRVPEPRLSNNECSC	81	
QY	64	LNERICLVGQCSTNSEKEPSILVEKICISPPGGDPESAVTELQCIWNLSYMKCSWLPG	123	
Db	82	TFREICLHEGVTFVHVNTSQRGFQQKLYPNSGREGTAAQNFCFIYNALMNCITWARG	141	
QY	124	RNTSPDNYTYLYWHRSLEKIHCENIFRE-QGYFCCSFD-LTKVKDSSEFHQSVOIMVK	181	
Db	142	PTAPRDVGQFYLI RNSKRRREIRCPYYTODSGTHVGCHLDNLUGTSRNY -----PLVN	195	

QY 182 DNAGKIKPSF--NIVPLTSRVKDDPPPHKXNLSFHNDDLLYVQWENPQNF--ISRCLP-YEV 236
Db 196 GTSREIGIQFDSLLDTKTKTERFNPNPNVTVCNTTCHLVKQRPYQKLSYLDQYQL 255
QY 237 EVN--NSQTEHNVFYVQEAACNPEPERNVENTSCFMVPGVLPDTLNVTVRIRVKNKLC 294
Db 256 DVHRKQTPQTEMLLINVSGLNLR-----YNFSSSPRAKSHVKIRAADVRIL 304
QY 295 YEDDKLWNWSQBSMSIGKKNSS--TLYITMLLIVPVIVAGAIIVLLYLKRLKI-IIPPP 351
Db 305 N-----WSSWSEAIKFGSDGNLGSVYIYVLLVIGTLVCG-IVLGFLEKRFALQRLFP 358
QY 352 IPPGKIFKMFQDN--DTLHWKXYDIYE-KQTKEETDSV 390
Db 359 VPQ-----IKDKJNDNHEVEDEIIWEETPEGRGYREELTV 396

RESULT 7
A55718
interleukin-2 receptor gamma chain precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A55718
R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.P.; Felsburg, P.
Genomics 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
A;Reference number: A55718; MUID:95130114; PMID:7829104
A;Accession: A55718
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P40321; UNIPARC:UPI00000128CA1; GB:U04361; NID:G517411; PIDN:
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication

Query Match 9.5%; Score 207; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 9.9e-09;
Matches 76; Conservative 52; Mismatches 131; Indels 44; Gaps 14;
QY 62 VPLNERICLVGSGCSTNESEKPSILVEKICSPPEGDPESAVTELOCIMHNLKMSW 121
Db 21 VGLNSTVPMNG-----NEDITDFLTATPSETLSVSSLPLEVCQFVFNVMCTWN 75
QY 122 PGRTSGPTNTLYYHRSI--EKIHQCN-IFREGQYFCGSPDLTKVKDSSFEQHSVQI 178
Db 76 SSSEPRP-TNLTLHYWYKNSNDKQVQECGYLFSREVTAGCW--LQKEETHLYETFFVQL 132
QY 179 MVKDNAGKIKPSNIVPLTSRVKEDDPHINKLSFHN-----DDLTVQWENPQNFISRCLFYE 235
Db 133 --RDPREPRQSTQKQLQNLVTPWAP--ENLTLNLSLSQSLWSN--RHLDHCLH 186
QY 236 VEYVNSQTETHNVFYVQEAACNPEPERNVENTSCFMVPGVLPDTLNVTVRIRVKNKLCY 295
Db 187 VQVRSWDRSWT-----EQSDVHRNSFLPSVDQKQYFFVRVRYPNLCG 232
QY 296 EDDKLWNWSQBSMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIFP 350
Db 233 SAQR-WSEWHPHWGNTSKENPLFASEAVLPLGSMGLISLICVYVWLER----SIP 287
QY 351 PIP 353
Db 288 RIP 290

RESULT 8
I49280
interleukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993

A;Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
A;Reference number: A47514; MUID:93391374; PMID:8378320
A;Accession: I49280
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369 <CAO>
A;Cross-references: UNIPROT:P34902; UNIPARC:UPI0000001949; EMBL:U21795; NID:G272349; PIDN:
A;Accession: A47514
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE2>
A;Cross-references: UNIPARC:UPI0000001949; GB:L20048; NID:G404067; PIDN:AAA39286.1; PID:G
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of functi
A;Reference number: JN0592; MUID:93277575; PMID:8503926
A;Accession: JN0592
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-369 <KUM>
A;Cross-references: UNIPARC:UPI0000001949; DDBJ:D13565; NID:G303684; PIDN:BAA02760.1; PI
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A;Reference number: JN0775; MUID:93366191; PMID:8359699
A;Accession: JN0775
A;Molecule type: mRNA
A;Residues: 1-369 <ROB>
A;Cross-references: UNIPARC:UPI0000001949; GB:D13821; NID:G436045; PIDN:BAA02974.1; PID:G
R;Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A;Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain.
A;Reference number: S37582
A;Accession: S37582
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A;Cross-references: UNIPARC:UPI0000176753; EMBL:X75337
R;DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A;Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal loc
A;Reference number: I53398; MUID:95104285; PMID:7805729
A;Accession: I53398
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369 <RES>
A;Cross-references: UNIPARC:UPI0000001949; GB:S75852; NID:G861554; PIDN:AAB32904.1; PID:G
C;Genetic:
A;Gene: IL-2Rgamma
A;Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C;Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (f
eptors.
C;Function:
A;Description: receptor for interleukin-2
A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F;256-284/Domain: transmembrane #status predicted <TM>
F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 205.5; DB 2; Length 369;
Best Local Similarity 24.0%; Pred. No. 1.3e-08;
Matches 76; Conservative 63; Mismatches 121; Indels 57; Gaps 16;
QY 77 STNESEKPSILVEKICSPPEGDPESAVTELOCIMHNLKMSWLPGRNTPD---TNYT 133
Db 31 SANEDIKADLILITSTAPEHLSAFTPLPEVCQFVFNIEYNNCTW----NSSSPQATNLT 86
QY 134 LYVWHRSLKIHQCNIFREGQYFCGSPDLTKVKDSSFEQHSVQ-----IMVKDNAGKI 187
Db 87 LHRYKVSVD-----NNTFQECSHYLFSEKIT--SGCQIQKEDIQLYQTVFVQLQDPQK 139

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QY 188 KPSNIVPLTSRVKPDPPHIKNLSFHN---DDLIVQHENPQNFISRCIFYEVEVNNQTE 244
Db 140 RRAVQKLNQNLVTPRAP--ENLTSLNSLSQELRWKS-RHIKERCLQVLDVQTRSNDR 196
QY 245 THNVFYQAEAKCENPEPERNVNVENTSCFVPGVLPDITLN--TVIRVTKNKLCEYEDDKLWS 302
Db 197 SWT-----ELIVNHEPRFSLPSV--DELKRYTFVRVSRVNPICGSSQ--WS 239
QY 303 NWQEMSIGK---KRNSTLYITMLIVPVIVAGAIIVLL---YLKRLKIIIFPPIDPPG 356
Db 240 KWSQPVHWSHTVEBNSLPALEAVLIPVGTMLGIITLIFYCWLERM-----PPIP-PI 293
QY 357 KIPKEMFGDQNDLTILHW 373
Db 294 KNLEDLVTEYQGNFSAW 310

RESULT 9
A2565
interleukin-2 receptor gamma chain - human
C/Species: Homo sapiens (man)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A42565; A46591; I54332
R/Takeshita, T.; Asao, H.; Ohtani, K.; Iehii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;
Science 257, 379-382, 1992
A/Title: Cloning of the gamma chain of the human IL-2 receptor.
A/Reference number: A42565; MUID:92335883; PMID:1631559
A/Accession: A42565
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid; protein
A/Cross-references: UNIPROT:P31785; UNIPARC:UPI0000000DEA; GB:D11086; NID:g303611; PIDN:
A/Experimental source: MOLT beta lymphoid cells
A/Note: sequence extracted from NCBI backbone (NCBIP:109167)
R/Nozuchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A/Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A/Reference number: A46591; MUID:93293887; PMID:8514792
A/Accession: A46591
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-369 <RES>
A/Cross-references: UNIPARC:UPI0000000DEA; GB:L12183; NID:g307056; PIDN:AAAS9145.1; PID:
R/Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He
Hum. Mol. Genet. 2, 1099-1104, 1993
A/Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link
A/Reference number: I54332; MUID:94004847; PMID:8401490
A/Accession: I54332
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-369 <RE2>
A/Cross-references: UNIPARC:UPI0000000DEA; GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:
C/Genetics:
A/Gene: GDB:IL2RG; SCIDX1; IMD4
A/Cross-references: GDB:I34807; OMIM:308380
A/Map position: Xq13.1-Xq13.1
A/Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A/Note: defects are associated with an X-linked form of severe combined immunodeficiency
C/Superfamily: interleukin-2 receptor gamma chain
C/Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 9.3%; Score 202; DB 2; Length 369;
Best Local Similarity 27.2%; Pred. No. 2.4e-08;
Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;
QY 105 ELQCIWHNLSYMKCSWLPGRNTPSDTNTLYTYWHRSLEKIHOCENIFREGQVFGCSF 161
Db 59 EYQCFVFNVEYMNCTWNSSESPQ--TNLTLYHYWYKNSDNKVKQKSHYLFSEITSGC-- 115
QY 162 DLTVKDSSFEQHSQVQIMVKONAGIKPSFNIVPLTSRVKPDPPHIKNLSFHN---NDLLY 218
Db 116 QLOKKEIHLHYQTFVQVQ---QDPREPRQATQMLKQNLVTPWAP--ENLTILKLSQLE 171
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QY 219 VOVENPQNFISRCI---FYEVEVNNQTEHNVFYVQAEAKCENPEPERNVNVENTSCFVMP 274
Db 172 LWNVN--RFLNHCLEHLVQRTDHSWT-----EQSDVYRHKFSLP 211
QY 275 GVLPDITLVTVIRVTKNKLCEYEDDKLWSNWSQMSIG---KRNSTLYITMLIVPVIVA 331
Db 212 SVDGQKRYTFVRVSRFNPLC-GSAQHWSEWSPHITHGNSNTSKENPFLFALEAVVISGSM 270
QY 332 GAIIVLL---LYLKLKLIIFPPIP 353
Db 271 GLIISLLCVTFWLER-----TMRPIP 291

RESULT 10
JQ1655
prolactin receptor precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JQ1655
R/Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A/Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A/Reference number: JQ1655; MUID:93075121; PMID:1445292
A/Accession: JQ1655
A/Molecule type: mRNA
A/Residues: 1-831 <TAN>
A/Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:g222848; PID
A/Experimental source: Kidney
C/Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
Query Match 9.1%; Score 197.5; DB 2; Length 831;
Best Local Similarity 23.1%; Pred. No. 1.6e-07;
Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;
QY 6 QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFHFQDKQKIAPEPTRR 59
Db 126 QPGSPV-NLTLETGRSANIMYLWAKWSPPLADASSN----HLVHY-----ELRIKPEKKE 176
QY 59 SIEVPLNERICLVGSGQCTNE-----SEKPSILVEKCI3PP 95
Db 177 EWET-----ISVGVTQCKINRLNAGMYVQVVRCTLDLPGSEWSEWSSERHILIPSGQSP 231
QY 96 EGDPESAVTELOCIWHNLSYMKCSWLPGRNTPSDTNTLYTYWHRSLEKIHOCENIFREGQ 155
Db 232 E-----KPTIIKCSPEKETTCWKPKDGDGHPNTYLLYSKEGEEQVYECPD-YRTAG 285
QY 156 YFGCSFDLTVKDSSFEQHSQVQIMVKONAGIKPSFNIVPLTSRVKPDPP-----HIKNL 210
Db 286 PNSCYFD--KKHTSFWTIYNTVRATNEMSGNSDPSHYVDVTYIVQDPVPVNVLELKKP 343
QY 211 SFHNDLLVQVENPQNFISR-----CLFYEVEVNNQTEHNVFYVQAEAKCENPEPERNVE 266
Db 344 INRKPYLVLTWSPPLADVRSGWLTLEYELRKPGESEWETIFVGQ-QTYQKMSLN-- 400
QY 267 NTSCFVPGVLPDITLVTVIRVTKNKLCEYEDDKLWSNWSQMSIGKKNSTLYITMLIV 326
Db 401 -----PGKKYIIQIHCKP-----DHHGSEWSESENIIQIPNDPRVKDMIVTV 444
QY 327 PVIAGAIIVLL---LYLKLKLIIF--PPIPDP 355
Db 445 LGVLSLLCLMSWTMLVKGYRMITFMLPPVGP 478

RESULT 11
A34631
lactogen receptor 1 - rat
```


C/Species: *Rattus norvegicus* (Norway rat)
C/Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C/Accession: A34631
R/Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A/Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A/Reference number: A34631; MUID: 90241201; PMID: 2159291
A/Accession: A34631
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-610 <ZRA>
A/Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170BE1; GB:M34083; NID:G205122; PIDN:
F/31-216/Domain: cytokine receptor homology <CRS>


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Db      219 SPSSIQIPNDFFPVKDTSMWIFVAILSAVICLINWVAVALKGYSMVTCILPPVPGP-KI- 27
Qy      360 KEMFGDQNDTTLHWKCKYDIY--EKOTKEE 386
Db      277 -----KGFVDVHLLERKSEE 291

Search completed: February 8, 2006, 22:07:07
Job time : 24.7733 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 21:53:18 ; Search time 139,493 Seconds
(without alignments)
2028.173 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172

Sequence: 1 APTETQPPVNLVSVENLC.....QTKEETDSVLIENLKASQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	1 I13R1_HUMAN	P78552 homo sapien
2	2172	100.0	427	2 Q5U516_XENLA	Q5U516 xenopus lae
3	2172	100.0	427	2 Q90XP8_ONCMY	Q90XP8 oncorhynchu
4	2159	99.4	426	2 Q15469_HUMAN	Q15469 homo sapien
5	2104	96.9	409	2 Q59EG2_HUMAN	P15509 homo sapien
6	1927	88.7	401	2 Q7YRV5_MACACA	Q4V311 homo sapien
7	1869	86.0	405	2 Q6U6T1_SHEEP	Q8NHV7 homo sapien
8	1859	85.6	423	2 Q95LPI_CANFA	Q4V312 homo sapien
9	1688	77.7	424	2 Q86326_PIG	Q66INI xenopus lae
10	1683	77.5	426	1 I13R1_MOUSE	Q76KDO sus scrofa
11	1682	77.5	424	2 Q561K3_RAT	Q8SQ71 sus scrofa
12	1672	77.0	424	2 Q8C123_MOUSE	Q68FUE rattus norv
13	1650	76.0	426	2 Q8BNM4_MOUSE	P40321 canis famil
14	1610	74.1	349	2 Q8VHC2_RAT	P34902 mus musculu
15	1387	63.9	279	2 Q9UDY5_HUMAN	Q8VHR8 rattus norv
16	977	45.0	252	2 Q8VDP7_MOUSE	
17	463	21.3	226	2 Q6ZM70_HUMAN	
18	318	14.6	415	1 ILERA_MOUSE	
19	310	14.3	386	1 I13R2_CANFA	
20	296	13.7	420	1 ILSRA_HUMAN	
21	294	13.6	380	1 I13R2_HUMAN	
22	294	13.6	420	2 Q14633_HUMAN	
23	287	13.2	383	2 Q88786_MOUSE	
24	282	13.0	396	2 Q14631_HUMAN	
25	279	12.9	415	2 Q920K4_CAVPO	
26	277	12.8	385	2 Q8VHK6_RAT	
27	273	12.6	414	2 Q920B8_RAT	
28	272	12.5	414	2 Q89PS3_RAT	
29	269	12.4	348	2 Q8AUP2_CHICK	
30	263	12.1	391	2 Q6UAN8_TEING	
31	262	12.1	374	2 Q8AV07_CHICK	

RESULT 1

ID I13R1_HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q95646; Q99656;
DT 01-NOV-1997 (Rel. 35, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen)
DB Name=I13RAL; Synonyms=IL13R, IL13RA;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., Ferrara P.;
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL [3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=F-cell;
RX MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;
RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13 receptor alpha chain."
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Pancreas;
RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.F., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
 CC can form a functional receptor for IL13. Also serves as an
 CC alternate accessory protein to the common cytokine receptor gamma
 CC chain for IL4 signaling, but cannot replace the function of gamma
 CC C in allowing enhanced IL2 binding activity.
 CC -I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
 CC and possibly other components.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
 CC skeletal muscle and ovary; lowest levels in brain, lung and
 CC kidney. Also found in B-cells, T-cells and endothelial cells.
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
 CC subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR ENBL; Y10659; CAA71669.1; -; mRNA.
 DR ENBL; Y09328; CAA70508.1; -; mRNA.
 DR ENBL; U62856; AAB37127.1; -; mRNA.
 DR ENBL; U81379; AAD00510.3; -; mRNA.
 DR ENBL; BC009560; AAH09560.1; -; mRNA.
 DR ENBL; ENSG00000131724; Homo sapiens.
 DR HGNC; HGNC:5974; IL13RA1.
 DR H-InvDB; HIX0017008; -.
 DR MIM; 300119; -.
 DR GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO REC_S_F2; 1.
 KW Glycoprotein; Receptor; signal; Transmembrane.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 427 Interleukin-13 receptor alpha-1 chain.
 FT TOPO_DOM 22 343 Extracellular (Potential).
 FT TRANSMEM 344 367 Potential.
 FT TOPO_DOM 368 427 Cytoplasmic (Potential).
 FT MOTIF 327 331 WSXWS motif.
 FT MOTIF 374 382 Box 1 motif.
 FT CARBOHYD 37 37 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 61 61 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 105 105 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 138 138 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 157 157 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 235 235 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 265 265 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 293 293 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 329 329 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 341 341 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 46 95 Potential.
 FT DISULFID 134 144 By similarity.

FT DISULFID 173 185 By similarity.
 FT CONFLICT 130 130 T -> I (in Ref. 3).
 FT CONFLICT 358 358 G -> D (in Ref. 3).
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 2172; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 4.9e-158;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 60
 DB |||||
 QY 27 APTETPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
 DB |||||
 QY 61 EVDLNERICLVQSCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
 DB |||||
 QY 87 EVDLNERICLVQSCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146
 DB |||||
 QY 121 LPCRNTSPDNTYLYWHRSLKIHOCENIFRGGQIFGCSFDLTWKVDSSFEGHSVQIMV 180
 DB |||||
 QY 147 LPCRNTSPDNTYLYWHRSLKIHOCENIFRGGQIFGCSFDLTWKVDSSFEGHSVQIMV 206
 DB |||||
 QY 181 KDNAGIKFSPNIVPLTSRVKPPPHIKNLSPFNDDLYVQWENPQNFISRCIFYEVVNN 240
 DB |||||
 QY 207 KDNAGIKFSPNIVPLTSRVKPPPHIKNLSPFNDDLYVQWENPQNFISRCIFYEVVNN 266
 DB |||||
 QY 241 SQTETNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 300
 DB |||||
 QY 267 SQTETNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCEYDDKL 326
 DB |||||
 QY 301 WSNWSQEMSTGKRNSTLYITMLIIVPVIIVAGAIIVLLLYLKLKLIIRPPIPDGKIFK 360
 DB |||||
 QY 327 WSNWSQEMSTGKRNSTLYITMLIIVPVIIVAGAIIVLLLYLKLKLIIRPPIPDGKIFK 386
 DB |||||
 QY 361 EMFGQNDQDTHLWKYDIYEKQTKETSDSVLLIENLKASQ 401
 DB |||||
 QY 387 EMFGQNDQDTHLWKYDIYEKQTKETSDSVLLIENLKASQ 427
 DB |||||
 RESULT 2
 Q5JSL4 HUMAN
 ID Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
 AC Q5JSL4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Interleukin 13 receptor, alpha 1.
 GN Name=IL13RA1; ORFNames=RPL13-12804.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC ENBL; AL391280; CAI41410.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003532; Hemtptnrecept_F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;
 Query Match 100.0%; Score 2172; DB 2; Length 427;

Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKQDKKIAPETRISI 60
Db 27 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKQDKKIAPETRISI 86

Qy 61 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146

Qy 121 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVDSSEFQHSVQIMV 180
Db 147 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVDSSEFQHSVQIMV 206

Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENQNFISRCIFYEVEVNN 266

Qy 241 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326

Qy 301 WSNWSQMSIGCKKNSTLYITMLLIVPVIIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 360
Db 327 WSNWSQMSIGCKKNSTLYITMLLIVPVIIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 386

Qy 361 EMFGQNDTTLHWKKYDIYKQTKETDSVVLLENLKKASQ 401
Db 387 EMFGQNDTTLHWKKYDIYKQTKETDSVVLLENLKKASQ 427

RESULT 3
ID Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.
AC Q96BB4_OAWX08;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E.,
RA Schnerfeld A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;

Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
DR EMBL: BC015768; AAH15768.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR002996; Cytokn_recept_B/G.
DR InterPro: IPR003532; Hemtptnrecept_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
DR Receptor; Transmembrane.
SQ SEQUENCE 427 AA; 48677 MW; 66A42F7466A39A09 CRC64;

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKQDKKIAPETRISI 60
Db 27 APTETQPPVNLVSVENLCTVIWTPNPPEGASNCSLWYFHFSGDKQDKKIAPETRISI 86

Qy 61 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGQCSNTESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 146

Qy 121 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVDSSEFQHSVQIMV 180
Db 147 LPGRNTSPDNTYLYWHRSLKIQHCENIFREQYFGCSFDLTWKVDSSEFQHSVQIMV 206

Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKNLSFHNDLLYVQWENQNFISRCIFYEVEVNN 266

Qy 241 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 300
Db 267 SQTETHNVFYVOEAKCENPEPERNVENTSCFMVPGVLPDNTLVIRVKTNKLCEYEDDKL 326

Qy 301 WSNWSQMSIGCKKNSTLYITMLLIVPVIIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 360
Db 327 WSNWSQMSIGCKKNSTLYITMLLIVPVIIVAGAIIVLLLYLKLKLIIFPPDPGKIFK 386

Qy 361 EMFGQNDTTLHWKKYDIYKQTKETDSVVLLENLKKASQ 401
Db 387 EMFGQNDTTLHWKKYDIYKQTKETDSVVLLENLKKASQ 427

RESULT 4
ID Q59EG2 HUMAN PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB209849; BAD93086.1; -; mRNA.


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121 LRGNTSPDNTYTLVHNSLGLKIQENIYREGQHIACSNLTAKVQSSFEQHSVQVMV 180
181 KDNAGKIKPSPNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
181 KDNAGKIRPSFNIVPLTSHVKPDPPHINKLSFQNGDLYVQWNTNPNFQSKLSYEVEVNN 240
241 SQTETHNVFVQAEKCNPRNVENTSCPMVPGVLPDNLTVIRVKTNKLCEYDDKL 300
241 SHAETHDIFVVEEAKCNTEFERNLEGTICPMVPGVLPDNLTVIRVKTNKLCEYDDKL 300
301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIPFPDPPGKIFK 360
301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIPFPDPPGKIFK 360
361 EMFGDQNDTLHWKKYDIYERQTKETDSSVLIENLKASQ 401
361 EMFGDQNDTLHWKKYDIYERQTKETDSSVLIENLKAAQ 401

RESULT 7
ID Q95LFI1 CANFA PRELIMINARY; PRT; 405 AA.
AC Q95LFI1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 13 receptor alpha chain 1 (Fragment).
GN Name=IL13R1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21287533; PubMed=11389954; DOI=10.1016/S0165-2427(01)00271-9;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
alpha2) cDNAs and detection of corresponding mRNAs in canine
tissues.";
RL Vet. Immunol. Immunopathol. 79:181-195 (2001).
DR EMBL; AF314532; AAL14886.1; -; mRNA.
DR Ensembl; ENSCARG0000018359; Canis familiaris.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemtpnrecept_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5B3F42 CRC64;

Query Match 86.0%; Score 1869; DB 2; Length 405;
Best Local Similarity 85.5%; Pred. No. 7.8e-135;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

QY 1 APTETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFQDKQDKKIAPETRISI 60
DB 5 APTETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFQDKQDKKIAPETRISK 64
QY 61 EVPLNERICLVQVSGQCSNTESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCSW 120
DB 65 EVPLNERICLVQVSGQCSNTESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCTW 124
QY 121 LPRGNTSPDNTYTLVYHRSLEKIHQENIFREGYFGCSFDLTAKVQSSFEQHSVQIMV 180
DB 125 LPRGNTSPDNTYTLVYHSSLGKILQCEDIYREGQHI GCSFALTNLKQSSFEQHSVQIMV 184
QY 181 KDNAGKIKPSPNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
```

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185 KDNARKIRPSFNIVPLTSHVKPDPPHINKLRFQNGNLYVQWKNPQNFYSRCLSYQVEVNN 244
241 SQTETHNVFVQAEKCNPRNVENTSCPMVPGVLPDNLTVIRVKTNKLCEYDDKL 300
245 SQTETNDIFVVEEAKCNSEFEGNLEGTICPMVPGVLPDNLTVIRVKTNKLCEYDDKL 304
301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIPFPDPPGKIFK 360
305 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLLKIIIPFPDPPGKIFK 364
361 EMFGDQNDTLHWKKYDIYERQTKETDSSVLIENLKASQ 401
365 EMFGDQNDTLHWKKYDIYERQTKETDSSVLIENLKASQ 405

RESULT 8
ID Q86326 PIG PRELIMINARY; PRT; 423 AA.
AC Q86326;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15350752; DOI=10.1016/j.vetimm.2004.05.003;
RA Zarlega D.S.; Dawson H.; Kringel H.; Solano-Aguilar G.;
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and
Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234 (2004).
CC -! SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -! DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
CC -! DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
DR EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003532; Hemtpnrecept_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 47984 MW; EA636FE6BCA533D9 CRC64;

Query Match 85.6%; Score 1859.5; DB 2; Length 423;
Best Local Similarity 85.0%; Pred. No. 4.4e-134;
Matches 341; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 1 APTETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFQDKQDKKIAPETRISI 60
DB 24 APAETQPPVTNLSVSNELCTVIWTWNPPEGASNCSLWYFSHFQDKQDKKIAPETRIS 83
QY 61 EVPLNERICLVQVSGQCSNTESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCSW 120
DB 84 EVPLNERICLVQVSGQCSNTESEKPSILVEKICSPPEGPESAVTELOCIWNHLSYMKCTW 143
QY 121 LPRGNTSPDNTYTLVYHRSLEKIHQENIFREGYFGCSFDLTAKVQSSFEQHSVQIMV 180
DB 144 LPRGNTSPDNTYTLVYHSSLGKILQCEDIYREGQHI GCSFALTNLKQSSFEQHSVQIMV 202
QY 181 KDNAGKIKPSPNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCIFYEVEVNN 240
```


Db 203 KDNAGKIRPAFISVPSSSHVKKPPPHIKLSFQNGDLYVQKNPQNFYSRCLSVQVEVNN 262

Qy 241 SQETHNVFVQAKCNPFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 300

Db 263 TQAKTHDIFVVEBAKQNSFEQNLGEMICFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 322

Qy 301 WSNWSQSMSTGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIPPIPDGKIFK 360

Db 323 WSNWSQSMSTGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIPPIPDGKIFK 382

Qy 361 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKASQ 401

Db 383 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKASQ 423

RESULT 9

IL13R1 MOUSE STANDARD; PRT; 424 AA.

AC OQ030; Q7TW27;

DT 01-NOV-1997 (Rel. 35, Last Created)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).

GN Name=IL13ral; Synonyms=IL13r, IL13ra;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN NUCLEOTIDE SEQUENCE.

RP MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;

RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A., Wilson T.A.;

RA "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.;"

RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).

RN [2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP STRAIN=FVB/N; TISSUE=Brain, and Colon;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -I- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling, but cannot replace the function of gamma C in allowing enhanced IL2 binding activity (By similarity).

CC -I- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1, and possibly other components (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney, testis, stomach, brain, skin, and colon; but not skeletal muscle.

CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein

CC folding and thereby efficient intracellular transport and cell-surface receptor binding.

CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or activation.

CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5 subfamily.

CC -----

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CC -----

DR EMBL; S80963; AAB50695.1; -; mRNA.

DR EMBL; BC052425; AAB52425.2; -; mRNA.

DR EMBL; BC059939; AAB59939.1; -; mRNA.

DR Ensembl; ENSMUSG0000017057; Mus musculus.

DR MGI; MGI:105052; Il13ral.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR002996; Cytok_recept_B/G.

DR InterPro; IPR003532; Hemtptnrecept_F2.

DR PROSITE; PS01356; HEMATOPO REC S F2; 1.

KW Glycoprotein; Receptor; Signal; Transmembrane.

FT SIGNAL 1 25 Potential.

FT CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.

FT TOPO_DOM 26 340 Extracellular (Potential).

FT TRANSMEM 341 364 Potential.

FT TOPO_DOM 365 424 Cytoplasmic (Potential).

FT MOTIF 324 328 WSXWS motif.

FT MOTIF 371 379 Box 1 motif.

FT CARBOHYD 35 35 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 103 103 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 136 136 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 262 262 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 338 338 N-linked (GlcNAc. .) (Potential).

FT DISULFID 44 93 Potential.

FT DISULFID 132 142 By similarity.

FT DISULFID 171 183 By similarity.

SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 77.7%; Score 1688.5; DB 1; Length 424;

Best Local Similarity 77.2%; Pred. No. 5.7e-121;

Matches 309; Conservative 40; Mismatches 150; Indels 1; Gaps 1;

Qy 1 APTETPPVNLVSVENICTVITWNPPEGASSNCLWVFSHFGDKQKIIAPETRRSI 60

Db 25 AATEVQPPVNLVSVENICTVITWNPPEGASSNCLWVFSHFGDKQKIIAPETHRKE 84

Qy 61 EYPLNERICLVQSGQCSSTNESEKPSILVEKICSPPEGDPESAVTELCIWHNLSYMKCSW 120

Db 85 ELPLDEKICLVQSGQCSANESKPSPLVKKICSPPEGDPESAVTELCIWHNLSYMKCSW 144

Qy 121 LFGRTNTPDNTLYIYWHRSLEKIHQCENI FREGQYFGCSFDLT VKDSSFEQHSVQIMV 180

Db 145 LFGRTNTPDNTLYIYWHRSLEKIHQCENI FREGQYFGCSFDLT VKDSSFEQHSVQIMV 203

Qy 181 KDNAGKIRPESFNI VPTSRVKPDPPHIKNLSFHNDLYVQWENPQNFISRCLEFYEVEVNN 240

Db 204 KDNAGKIRPESFNI VPTSRVKPDPPHIKNLSFHNDLYVQWENPQNFISRCLEFYEVEVNN 263

Qy 241 SQETHNVFVQAKCNPFERNVENTSCFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 300

Db 264 TQAKTHDIFVVEBAKQNSFEQNLGEMICFMVPGVLPDTLNTVRIRVTKNKLCEYEDDKL 323

Qy 301 WSNWSQSMSTGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIPPIPDGKIFK 360

Db 324 WSNWSQSMSTGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIPPIPDGKIFK 383

Qy 361 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKAS 400

Db 384 EMFGDQNDTLHWKKYDIYEKQKEETDSVVLLENLKKAS 423


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123 GRNTSPDNTNTLYWHRSLKIHOCENIFREGQYFGCSFDLTCKVDSFSEQHSVQIMVKD 182
147 GKNTSPDNTNTLYWYSSLSKLOECENIHREGQHIGCSFKLTKV-ESNYEHNHNIQIMVKD 205
183 NAGKIPSFNIVPLTSRVKDDPPHINKLSFNHNDLLYQWENPQNFISRLCYEYEVNNSQ 242
206 NAGKIRPSYKIVSFTSNVKGPPHKKHLFKNGALFQWKNPQNFSSRCLSYEYEVNSTQ 265
243 TETH--NVFVYQEAQENPFRNVENTSCFMVGLVPLDTLNTVRIRVKTNKLCEVDDKL 300
266 TDSYNSLSLEVEDKQNSFDRNNEGASCISFGLVANTVTVVRVKTNKLCEVDDNDL 325
301 WSNWSQMSIGCKKNSTLYITMLIIVPVIAGAIIVLLLYLKLRLKIIFPPPIPPGKIPK 360
326 WSNWSEALSIGKFNSTFYITMLIIPVFAVAVIILLFYLKRLKIIFPPPIPPGKIPK 385
361 EMFGDQDDTLHWKKYDIYEKQTEEDTSVVLLENLKKAS 400
386 EMFGDQDDTLHWKKYDIYEKQTEEDTSVVLLENLKKAA 425

RESULT 11
Q8C1Z3 MOUSE
ID Q8C1Z3 MOUSE PRELIMINARY; PRT; 424 AA.
AC 08C1Z3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus embryo RCB-0549 Cle-H3 CDNA, RIKEN full-length enriched
DE library, clone:G430044106 product:interleukin 13 receptor, alpha 1,
DE full insert sequence.
GN Name=Il13ral;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Anoh H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA The FANTOM Consortium,

```


QY 123 GRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSEFQHSVOIMVKD 182
 DB 147 GRNTSPDNTYLYYWSLGSKSLCQENIHRGQHGHSFKUTKV-ESNYEHNNIOMVKD 205
 QY 183 NAGKIKPSFNIVPLTSRVKPPDPPIKNSLFNDLTYQWENPQNFISRCIFYEVEVNSQ 242
 DB 206 NAGKIRPSYKIVTSFNVPKPPPHIKHLFLKNGALFVQKNQPNFSSRCLSYEVEVNSTQ 265
 QY 243 TETH--NVFYVQKACNPEPERNVENTSCFMVPGVLPDNTLVTRIRVKTNKLKYEDDKL 300
 DB 266 TDSYNSNSLEVEDKQNSFDRNMEGASCFISPGVLANTVYTVRVKTNKLCFDDNDL 325
 QY 301 WSNWSQMSIGCKNSLYITMLIVPVIVAGAIIVLLLYLKRKLIIFPPPIPPGKIFK 360
 DB 326 WSNWSALSIGKPSNSTFYITMLLIIPVFAVAVIILLFYLKRKLIIFPPPIPPGKIFK 385
 QY 361 EMFGDQNDTLHWKKYDIYEKQTEEDSVVLIENLKKA 400
 DB 386 EMFGDQNDTLHWKKYDIYEKQTEEDSVVLIENLKKA 425
 RESULT 14
 O97597 BOVIN
 ID O97597 BOVIN PRELIMINARY; PRT; 349 AA.
 AC O97597;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Interleukin-13 receptor alpha-1 chain (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=2008132; PubMed=10614495; DOI=10.1016/S0165-2427(99)00117-8;
 RX Trigona W.L., Brown W.C., Estes D.M.;
 RT "Functional implications for signaling via the IL4R/IL13R complex on
 bovine cells.";
 RL Vet. Immunol. Immunopathol. 72:73-79 (1999).
 DR EMBL; AF074402; AAC98147.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytokn recept B/G.
 DR InterPro; IPR003532; Hemtptnrecept F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT TER 349 349
 SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;
 Query Match 74.18; Score 1610; DB 2; Length 349;
 Best Local Similarity 84.5%; Pred. No. 4.6e-115;
 Matches 295; Conservative 17; Mismatches 37; Indels 0; Gaps 0;
 QY 9 VTNLVSVENLCTVIWTPNPEGASNCSLWYFSHFGDKQDKKIAPETRISIEVPLNERI 68
 DB 1 VTNLVSVENLCTVIWTPNPEGASNCSLWYFSHFGDKQDKKIAPETRISIEVPLNERI 60
 QY 69 CLQVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSWLPGRNTSP 128
 DB 61 CLQVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSWLPGRNASP 120
 QY 129 DTYNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSEFQHSVOIMVKDNGKIK 198
 DB 121 DPNYLYYWHNSLGKILQCCNFYREGQHIACSFNLTWKVDSSEFQHSVOIMVKDNGKIS 180
 QY 189 PSFNIVPLTSRVKPPDPPIKNSLFNDLTYQWENPQNFISRCIFYEVEVNSOTETHNV 248
 DB 181 PSFNIVPLTSRVKPPDPPIKNSLFNDLTYQWENPQNFISRCIFYEVEVNSHAETHDI 240

QY 249 FYVQKACNPEPERNVENTSCFMVPGVLPDNTLVTRIRVKTNKLKYEDDKLWSNWSQEM 308
 DB 241 FYVEAKQCNTEFEGNLEGICFMVPGVLPDNTLVTRIRVKTNKLKYEDDKLWSNWSQAM 300
 QY 309 SIGCKRNSLYITMLIVPVIVAGAIIVLLLYLKRKLIIFPPPIPPGK 357
 DB 301 SIGCKANQTYITMLLIIPVIVAAVIVLLLYLKRKLIIFPPPIPPGK 349
 RESULT 15
 O9UDY5_HUMAN
 ID O9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
 AC O9UDY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
 1).
 GN Name=IL13RA1; ORFNames=RP13-12804.2-002;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wada M., Hisano T., Kuwano M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation (By similarity).
 DR EMBL; U81380; RAD00511.2; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002996; Cytokn recept B/G.
 DR InterPro; IPR003532; Hemtptnrecept F2.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 279 AA; 31659 MW; E74141F99F8E9EBB CRC64;
 Query Match 63.9%; Score 1387; DB 2; Length 279;
 Best Local Similarity 99.6%; Pred. No. 4.4e-98;
 Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APTETPPVTNLVSVENLCTVIWTPNPEGASNCSLWYFSHFGDKQDKKIAPETRISI 60
 DB 27 APTETPPVTNLVSVENLCTVIWTPNPEGASNCSLWYFSHFGDKQDKKIAPETRISI 86
 QY 61 EVPLNERICLOVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
 DB 87 EVPLNERICLOVGSQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
 QY 121 LPGRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSEFQHSVOIMV 180
 DB 147 LPGRNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSEFQHSVOIMV 206
 QY 181 KDNAGKIKPSFNIVPLTSRVKPPDPPIKNSLFNDLTYQWENPQNFISRCIFYEVEVNN 240
 DB 207 KDNAGKIKPSFNIVPLTSRVKPPDPPIKNSLFNDLTYQWENPQNFISRCIFYEVEVNN 266
 QY 241 SQTEHNVFYVQ 252
 DB 267 SQTEHNVFYVQ 278

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Job time : 140.493 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:06:20 ; Search time 33.2127 Seconds
(without alignments)
998.200 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172
Sequence: 1 APTETQPPVTNLSVSVENLCL.....QTKETDSVVLNKKASQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	426	2	US-09-688-286D-4
2	2172	100.0	427	2	US-08-969-125-9
3	2172	100.0	427	2	US-09-545-002-9
4	2172	100.0	427	2	US-09-949-016-6094
5	1869	86.0	405	2	US-09-828-995B-50
6	1749.5	80.5	784	2	US-09-313-942-30
7	1749.5	80.5	784	2	US-10-282-162-30
8	1745	80.3	322	2	US-09-825-561A-82
9	1745	80.3	793	2	US-09-313-942-32
10	1745	80.3	793	2	US-10-282-162-32
11	1688.5	77.7	424	2	US-09-688-286D-2
12	1265	58.2	233	1	US-09-949-016-8550
13	318	14.6	398	1	US-07-757-390-6
14	318	14.6	398	1	US-08-442-282-6
15	318	14.6	398	1	US-08-442-281-6
16	318	14.6	398	1	US-08-939-727-6
17	318	14.6	415	1	US-07-757-390-5
18	318	14.6	415	1	US-08-442-282-5
19	318	14.6	415	1	US-08-442-281-5
20	318	14.6	415	1	US-08-939-727-5
21	318	14.6	415	2	US-09-886-319A-23
22	310	14.3	365	2	US-09-828-995B-66
23	310	14.3	386	2	US-09-828-995B-61
24	304.5	14.0	561	2	US-09-828-995B-72
25	303.5	14.0	561	2	US-09-828-995B-81
26	297	13.7	565	2	US-09-828-995B-75
27	296.5	13.7	420	2	US-09-886-319A-24

28	296.5	13.7	420	2	US-09-949-016-5958	Sequence 5958, Ap
29	296	13.6	318	2	US-09-828-995B-69	Sequence 69, Appl
30	296	13.6	563	2	US-09-828-995B-78	Sequence 78, Appl
31	294.5	13.6	380	1	US-08-609-572-4	Sequence 4, Appl
32	294.5	13.6	380	2	US-08-841-751-4	Sequence 4, Appl
33	294.5	13.6	380	2	US-08-846-340-4	Sequence 4, Appl
34	294.5	13.6	380	2	US-08-846-344-4	Sequence 4, Appl
35	294.5	13.6	380	2	US-09-301-808-4	Sequence 4, Appl
36	294.5	13.6	420	1	US-07-757-390-13	Sequence 13, Appl
37	294.5	13.6	420	1	US-08-442-282-13	Sequence 13, Appl
38	294.5	13.6	420	1	US-08-442-281-13	Sequence 13, Appl
39	294.5	13.6	420	1	US-08-939-727-13	Sequence 13, Appl
40	293.5	13.5	427	2	US-09-949-016-8614	Sequence 8614, Ap
41	293.5	13.5	427	2	US-09-949-016-8620	Sequence 8620, Ap
42	287.5	13.2	383	1	US-08-609-572-2	Sequence 2, Appl
43	287.5	13.2	383	2	US-08-841-751-2	Sequence 2, Appl
44	287.5	13.2	383	2	US-08-846-340-2	Sequence 2, Appl
45	287.5	13.2	383	2	US-08-846-344-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

Query Match	100.0%	Score 2172;	DB 2;	Length 426;			
Best Local Similarity	100.0%	Pred. No. 6.4e-212;					
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0			
Qy	1	APTETQPPVTNLSVSVENLCTVIWTNPP	EGASSNC	SLWYFSHF	GDKQDKKI	APTRRSI	60
Db	26	APTETQPPVTNLSVSVENLCTVIWTNPP	EGASSNC	SLWYFSHF	GDKQDKKI	APTRRSI	85
Qy	61	EYPLNERICLVGSCQSTNESEKPSILVEKICISPP	EGDP	PESAVTELCI	WHNLSYMKCSW	120	
Db	86	EYPLNERICLVGSCQSTNESEKPSILVEKICISPP	EGDP	PESAVTELCI	WHNLSYMKCSW	145	
Qy	121	LPGRNTSPDTNLTLYWHSRLEKIHOCENIFREGQY	FGCSFDLTKVKQSS	FEQHSVQIMV	180		
Db	146	LPGRNTSPDTNLTLYWHSRLEKIHOCENIFREGQY	FGCSFDLTKVKQSS	FEQHSVQIMV	205		
Qy	181	KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFN	DDLYVQWENPQNFISRCIFYEVEVNN	240			
Db	206	KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFN	DDLYVQWENPQNFISRCIFYEVEVNN	265			
Qy	241	SOTETHNVFYQEA	CENPEFERNVENTSCFMP	VGVLPTDLTNTVIRVTKNLCYEDDKL	300		

Db 266 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLKYEDDKL 325
QY 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 326 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 385
QY 361 EMFGDQNDTLHWKXYDIYEKQTEETSDSVLIENLKASQ 401
Db 386 EMFGDQNDTLHWKXYDIYEKQTEETSDSVLIENLKASQ 426

RESULT 2
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-No. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-212;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 27 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146
QY 121 LPRGNTSPDNTLYTYWHRSLKIHQCENTFREGQYFGCSFDLTVKVQSSFEQHSQIMV 180
Db 147 LPRGNTSPDNTLYTYWHRSLKIHQCENTFREGQYFGCSFDLTVKVQSSFEQHSQIMV 206
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFVEVEVNN 240

Db 207 KONAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFVEVEVNN 266
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLKYEDDKL 300
Db 267 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLKYEDDKL 326
QY 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 386
QY 361 EMFGDQNDTLHWKXYDIYEKQTEETSDSVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKXYDIYEKQTEETSDSVLIENLKASQ 427

RESULT 3
US-09-545-002-9
; Sequence 9, Application US/09545002
; Patent No. 6743604
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,002
; FILING DATE: 12-No. 6743604-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125
; FILING DATE: 12-No. 6743604-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-002-9

Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-212;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
Db 27 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 86
QY 61 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVQSGSQSTNESEKPSILVEKICISPPGDPESAVTELQCIWHNLSYMKCSW 146

Qy 121 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 147 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 206
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 326
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 427
RESULT 4
US-09-949-016-6094
; Sequence 6094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6094
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6094
Query Match 100.0%; Score 2172; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 6,4e-212; Mismatches 0; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 60
Db 27 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICSPPEGDPESAVTELOCIVHNLKSYMKCSW 120
Db 87 EVPLNERICLVGSCQSTNESEKPSILVEKICSPPEGDPESAVTELOCIVHNLKSYMKCSW 146
Qy 121 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 147 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 206
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 240
Db 207 KDNAGKIKPSFNIIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 266
Qy 241 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 300
Db 267 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 326
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 386

Qy 361 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 401
Db 387 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 427
RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50
Query Match 86.0%; Score 1869; DB 2; Length 405;
Best Local Similarity 85.5%; Pred. No. 3,7e-181; Mismatches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;
Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSTLRYPFSGDKQDKKIAPETRHSK 64
Qy 61 EVPLNERICLVGSCQSTNESEKPSILVEKICSPPEGDPESAVTELOCIVHNLKSYMKCSW 120
Db 65 EVPLNERICLVGSCQSTNESEKPSILVEKICSPPEGDPESAVTELOCIVHNLKSYMKCTW 124
Qy 121 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 125 LPGRNTSPDNTLYYYHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 184
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCIFYEVEVNN 240
Db 185 KDNARKIRPSFNIIVPLTSRVKPPPHIKRLFPQNGNLYVQWKNPQNFYSRCLSYQVEVNN 244
Qy 241 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 300
Db 245 SQTETHNVFYVQEAACENPEERNVENTSCFMVPGVLPDNTLVIRVTKNKLCEYEDDKL 304
Qy 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 360
Db 305 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 364
Qy 361 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 401
Db 365 EMFGDQNDTLHWKYYDIYEKQTKETSDSVVLIENLKASQ 405
RESULT 6
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942

		CURRENT FILING DATE: 1999-05-19			
		PRIOR APPLICATION NUMBER: 09/313,942			
		PRIOR FILING DATE: 1999-05-19			
		PRIOR APPLICATION NUMBER: 60/101,858			
		PRIOR FILING DATE: 1998-09-25			
		NUMBER OF SEQ ID NOS: 32			
		SOFTWARE: FastSeq for Windows Version 3.0			
		SEQ ID NO 30			
		LENGTH: 784			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-313-942-30			
		Query Match 80.5%; Score 1749.5; DB 2; Length 784;			
		Best Local Similarity 90.5%; Pred. No. 1.4e-168;			
		Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;			
Qy	1	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	60		
Db	239	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	238		
Qy	61	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	120		
Db	299	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	358		
Qy	121	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	180		
Db	359	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	418		
Qy	181	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	240		
Db	419	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	478		
Qy	241	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	300		
Db	479	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	538		
Qy	301	WSNWSQEMSIGKGRNST-----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP	353		
Db	539	WSNWSQEMSIGKGRNSTTGDKTHTCPAPPELLGGP-----SVFLFPPKP	584		
		RESULT 7			
		US-10-282-162-30			
		Sequence 30, Application US/10282162			
		Patent No. 6927044			
		GENERAL INFORMATION:			
		APPLICANT: REGENERON PHARMACEUTICALS, INC.			
		TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING			
		FILE REFERENCE: REG 203-B-US			
		CURRENT APPLICATION NUMBER: US/10/282,162			
		PRIOR FILING DATE: 2002-10-28			
		PRIOR FILING DATE: 1999-09-22			
		PRIOR FILING DATE: 1999-09-22			
		PRIOR FILING DATE: 1999-09-22			
		NUMBER OF SEQ ID NOS: 56			
		SOFTWARE: FastSeq for Windows Version 3.0			
		SEQ ID NO 30			
		LENGTH: 784			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-10-282-162-30			
		Query Match 80.5%; Score 1749.5; DB 2; Length 784;			
		Best Local Similarity 90.5%; Pred. No. 1.4e-168;			
		Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;			
Qy	1	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	60		
Db	239	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	238		
Qy	61	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	120		
Db	299	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	358		
Qy	121	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	180		
Db	359	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	418		
Qy	181	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	240		
Db	419	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	478		
Qy	241	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	300		
Db	479	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	538		
Qy	301	WSNWSQEMSIGKGRNST-----LYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIP	353		
Db	539	WSNWSQEMSIGKGRNSTTGDKTHTCPAPPELLGGP-----SVFLFPPKP	584		
		RESULT 8			
		US-09-825-561A-82			
		Sequence 82, Application US/09825561A			
		Patent No. 6777539			
		GENERAL INFORMATION:			
		APPLICANT: Sprecher, Cindy A.			
		APPLICANT: No. 6777539ak, Julia E.			
		APPLICANT: West, James W.			
		APPLICANT: Presnell, Scott R.			
		APPLICANT: Holly, Richard D.			
		APPLICANT: Nelson, Andrew J.			
		TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS			
		FILE REFERENCE: 00-22			
		CURRENT APPLICATION NUMBER: US/09/825,561A			
		CURRENT FILING DATE: 2000-04-05			
		PRIOR FILING DATE: 2000-04-05			
		PRIOR FILING DATE: 2000-07-28			
		NUMBER OF SEQ ID NOS: 86			
		SOFTWARE: FastSeq for Windows Version 3.0			
		SEQ ID NO 82			
		LENGTH: 322			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-825-561A-82			
		Query Match 80.3%; Score 1745; DB 2; Length 322;			
		Best Local Similarity 100.0%; Pred. No. 1e-168;			
		Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	60		
Db	6	APTETQPPVTLNLSVSVENLCTVIWTPNPPGASSNCSLWYFHFHFGDKQDKKIAPETRRSI	65		
Qy	61	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	120		
Db	66	EVLNERICLVGSCQSTNESEKPSILVEKICISPPGDPDESATVTELCIWHNLSYMKCSW	125		
Qy	121	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	180		
Db	126	LPGRNTSPDTNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIIMV	185		
Qy	181	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	240		
Db	186	KONAGKIKPSFNIVPLTSRVKDPDPHINKLSFNHDDLQYQWENPQNFISRCCLFYEVVNN	245		
Qy	241	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	300		
Db	246	SQTEHNVFVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLQCYEDDKL	305		
Qy	301	WSNWSQEMSIGKGRNST 317			

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; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

Query Match      80.3%; Score 1745, DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.1e-168;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  APTETOPPVTNLSVSENLCVTWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 60
Db  27  APTETOPPVTNLSVSENLCVTWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI 86

Qy  61  EVLNRIICLOVGSQCSTNSESEKPSILVEKCIISPPEGDPESA VTQLCIIWHNLSYMKCSW 120
Db  87  EVLNRIICLOVGSQCSTNSESEKPSILVEKCIISPPEGDPESA VTQLCIIWHNLSYMKCSW 146

Qy  121  LPRGNTSPDNTYLYYWHRSLEKIHQCENTFRGQYFGCSFDLTKVXDSSEFQHSVQIMV 180
Db  147  LPRGNTSPDNTYLYYWHRSLEKIHQCENTFRGQYFGCSFDLTKVXDSSEFQHSVQIMV 206

Qy  181  KDNAGIKPSFNIVPLTSRVKPPDPPIKNLSFHNDDLYVQWENPQNFI SRCLFYEVEVNN 240
Db  207  KDNAGIKPSFNIVPLTSRVKPPDPPIKNLSFHNDDLYVQWENPQNFI SRCLFYEVEVNN 266

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267 SQETHNVFVQEA KENP ERFENVNTSCFMVPGVLPDTLNTVIRVKNKLCYEDDKL 326
301 WSNWSQEMSGKKRNST 317
327 WSNWSQEMSGKKRNST 343

RESULT 11
US-09-688-286D-2
; Sequence 2, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola , Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang , Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences enc
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688, 286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-286D-2

Query Match      77.7%; Score 1688.5; DB 2; Length 424;
Best Local Similarity 77.2%; Pred. No. 8.6e-163;
Matches 309; Conservative 40; Mismatches 50; Indels 1; Gaps 1

QY    1 APTQTQPVTNLSVSNELCTVIWTWMPPEGASNCSLMWYFSHFQDKODKKIAPETRRSI 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB    25 AAATEVQPVTNLSVSNELCTIIWTWSPPEGASPNCITLYRFSHFDDQQDKKIAPETHRKE 84
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY    61 EVPNLERICLQVGQCSTNESEKPSILYEKCISPPGDPESANVFLOCIWNLSYMKCSW 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 85 ELPLDEKICLVQGSQCSANESEKPSPLVKKCISPPGDPESAVTELKCIWHNLSYMKCSW 144
Qy 121 LPGNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 180
Db 145 LPGNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSSFEQHSVQIMV 203
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFSRCLFYEVEVNN 240
Db 204 KDNAGKIRPCKIVSLTSYVKPDPPHINKNLSFHNDLLVQWENPQNFSRCLFYEVEVNN 263
Qy 241 SQTETHNVFVQEAACENPERFVENTSCFMVPGVLPDNTLVIRVKTNKLCEYDDKL 300
Db 264 TQTDHNLVEEDKQCSSEDRNMGCTSCFQLPGLADAVYTVRVKTNKLCFDNKL 323
Qy 301 WSNWSQEMSGKGRNSTLYTMLIVPVIVAGAIIVLLLYLKRKIIIFPPIDPDGKIFK 360
Db 324 WSDWSEASQSIGKEQNSTFYTMLITIPFVAVAVIILLFYLKRLKIIFPPIDPDGKIFK 383
Qy 361 EMFGDQNDTLHWKXYDIYEKOTKEETDSVLIENLAKAS 400
Db 384 EMFGDQNDTLHWKXYDIYEKQSBETDSVLIENLAKAA 423

RESULT 12

US-09-949-016-8550
; Sequence 8550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8550
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8550

Query Match 58.2%; Score 1265; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 3.8e-120;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 KIAPETRRSIEVPLNERICLVQGSQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCQIW 110
Db 1 KIAPETRRSIEVPLNERICLVQGSQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCQIW 60
Qy 111 HNLISYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSS 170
Db 61 HNLISYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFREGQYFGCSFDLTWKVDSS 120
Qy 171 FEQHSVQIMVKDAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFSR 230
Db 121 FEQHSVQIMVKDAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLVQWENPQNFSR 180
Qy 231 CLFYEVEVNNQSQTETHNVFVQEAACENPERFVENTSCFMVPGVLPDNTLVIRVKT 281
Db 181 CLFYEVEVNNQSQTETHNVFVQEAACENPERFVENTSCFMVPGVLPDNTLVIRVKT 231

RESULT 13

US-07-757-390-6
; Sequence 6, Application US/07757390
; Patent No. 5453491

; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-6

Query Match 14.6%; Score 318; DB 1; Length 398;
Best Local Similarity 23.9%; Pred. No. 1.5e-23;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

Qy 7 PVTNLSVSVENLCTVIWITWNP-PGASSNCSLWYFSHP-GDKQDKKIAPETRRSIEVPL 64
Db 12 PPV-NFTIKATGLAQVLLHWDPNPQEQRHVDLEYHVKINAPQEDBYDTRKTESKCVTPL 70
Qy 65 NERICLVQGSQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCQIWHNL----- 113
Db 71 HEGFAASVRTLKSSHTTLASSWVSAELKAPPGSGTSTNLTCTTHTTVVSSHTRLPYQ 130
Qy 114 SYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQCNIFRE--GOYFGCSFDLTWKVDSSF 171
Db 131 VSLRCTLWKGDAPEDTQFLYRFGVLTE--KCQYSRDALNRNTACTWPRTFINSKGF 188
Qy 172 EQHSVQIMVKDAGKIKPSFNIVPLTSRVKPDPPHINKNLSFHNDLLVQWENPQN-FISR 230
Db 189 EQLAVHINGSKRAAIKPPDQLFSLAIDQVNPVRNVTVIESNSLYIQWEKPLSAPPDH 248
Qy 231 CLFYEVEVNNQSQTETHNVFVQEAACENPERFVENTSCFMVPGVLPDNTLVIRVKT 290
Db 249 CFNYELKIYNTKNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAAV 292
Qy 291 NKLCEYBDDKLSNWSQEMSGKGRNSTLYTMLIVPVIVAGAIIVLLLYLKRKIIIFPP 347
Db 293 SSFCRMPGR-WGWSQPIYVGERKS-LVENHLIVLP--TAACFVLLIFSLICRVCHLW 347
Qy 348 --IFPPIDPDGKIKFEMFGDQNDTLHWKXYDIYEKOTKEETDSV 391
Db 348 TRLFPVPVPAPKSNIKDL-----PVTVEYKPSNETKIEV 382

Query Match	14.6%;	Score 118;	DB 1;	Length 398;
Best Local Similarity	23.9%;	Pred. No. 1.5e-23;		
Matches	97;	Conservative 74;	Mismatches 179;	Indels 56; Gaps 14;
Qy	7	PPVTNLVSVENLCTVIWTNP-PEGASSNSCLMYFSHF-GDKQDKKIAPETRRESIEVPL	64	
Db	12	PPV-NFTIKATGLAQVLLHWDPNPDQQRHVDLEYHVKINAPQDEYDTRKTESKCVTL	70	
Qy	65	NERICLQVGSOCSTNESKSPILVEKICISPEGPDESATVLOCLIHNL	113	
Db	71	HEGPAASVRTIKLSHTTSLASSWSYSAELKAPPGSGTSTNLCTTHTVWSSHTRLRPYQ	130	
Qy	114	SYMCKSLPGRSTPDNTYTLYYHRSLEKIHOCENIRE--GOYFGCSFOLTKVKOSSF	171	
Db	131	VSLRCTLVLGKDAPEDTQYFLYYRFGVUTE--KQEYSRDLNRNTACWFRTFINSKGF	188	
Qy	172	EQHSVQIMVKDNAGKIKPSFNIVLTSRVKPDPPHINKLSFHNDDLYVQWENPON-FISR	230	
Db	189	EQLAVHINGSSKRAAIKPFQDLFSLDAIQVNPPRNVTVIESNSLYIQWEKPLSAFPDH	248	
Qy	231	CLFVEVEVNNSGTETHNVFYVQEAECENPERERNVENTSCFWPGVLDTLNTVIRVKT	290	
Db	249	CFNYELKITYNKG-----HIQKEKLIANKPISKIDDVSTY-----SIQVRAAV	292	
Qy	291	NKLCYEDDKLNSNWOEMSIGKRRNSTLYITMLTIVPVIVAGAIIVLLLYLKRKII---	347	

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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:28:54 ; Search time 108.728 Seconds
(without alignments)
1540.998 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172
Sequence: 1 APTETQPPVTNLSVSNELCTVIWNPPEGASNCSLWYFHFSGDKQDKKIAPETRRSI 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	4	US-10-671-697-9
2	2172	100.0	427	6	US-11-067-251-3
3	2165	99.7	427	5	US-10-850-270-4
4	2154	99.2	426	4	US-10-036-568-4
5	1869	86.0	405	3	US-09-828-995B-50
6	1869	86.0	405	4	US-10-753-159-50
7	1784.5	82.2	664	5	US-10-850-270-10
8	1750	80.6	776	3	US-09-935-868-36
9	1749.5	80.5	784	3	US-09-313-942-30
10	1749.5	80.5	784	3	US-09-935-868-30
11	1749.5	80.5	784	4	US-10-287-035-30
12	1749.5	80.5	784	4	US-10-282-162-30
13	1749.5	80.5	784	6	US-11-134-114-30
14	1745	80.3	322	3	US-09-825-561A-82
15	1745	80.3	322	5	US-10-872-087-82
16	1745	80.3	322	5	US-09-935-868-34
17	1745	80.3	793	3	US-09-313-942-32
18	1745	80.3	793	3	US-09-935-868-32
19	1745	80.3	793	4	US-10-287-035-32
20	1745	80.3	793	4	US-10-282-162-32
21	1745	80.3	793	6	US-11-134-114-32
22	1741	80.2	776	3	US-09-935-868-44
23	1741	80.2	776	4	US-10-287-035-40
24	1741	80.2	776	6	US-11-067-251-8
25	1741	80.2	776	6	US-11-067-251-10
26	1741	80.2	776	6	US-11-067-251-12
27	1741	80.2	776	6	US-11-067-251-14

28	1741	80.2	776	6	US-11-067-251-16
29	1740	80.1	776	3	US-09-935-868-40
30	1736	79.9	778	3	US-09-935-868-46
31	1736	79.9	778	4	US-10-287-035-46
32	1736	79.9	778	4	US-10-287-035-60
33	1736	79.9	780	3	US-09-935-868-42
34	1736	79.9	782	3	US-09-935-868-50
35	1735	79.9	778	3	US-09-935-868-58
36	1735	79.9	778	4	US-10-287-035-50
37	1735	79.9	778	4	US-10-287-035-56
38	1735	79.9	780	3	US-09-935-868-38
39	1735	79.9	782	3	US-09-935-868-52
40	1732	79.7	776	4	US-10-287-035-44
41	1731.5	79.7	780	4	US-10-287-035-34
42	1731	79.7	776	4	US-10-287-035-36
43	1722.5	79.3	780	4	US-10-287-035-42
44	1722.5	79.3	782	4	US-10-287-035-48
45	1722.5	79.3	782	4	US-10-287-035-54

ALIGNMENTS

RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/671,697
; FILING DATE: 29-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/545,002
; FILING DATE: 06-APR-2000
; APPLICATION NUMBER: US 08/969,125
; FILING DATE: 12-NOV-1997
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9

Query Match	100.0%	Score	2172	DB 4	Length	427	
Best Local Similarity	100.0%	Pred. No.	7.8e-180	Indels	0	Gaps	0
Matches	401	Conservative	0	Mismatches	0		
Qy	1	APTETQPPVTNLSVSNELCTVIWNPPEGASNCSLWYFHFSGDKQDKKIAPETRSI 60					
Db	27	APTETQPPVTNLSVSNELCTVIWNPPEGASNCSLWYFHFSGDKQDKKIAPETRSI 86					
Qy	61	EVLNERICLVGSCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120					

Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 401
Db 387 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 427

RESULT 2

US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien

US-11-067-251-3

Query Match 100.0%; Score 2172; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 7,8e-180;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETOPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRI 60
Db 27 APTETOPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRI 86
Qy 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326

Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 401
Db 387 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 427

RESULT 3

US-10-850-270-4
; Sequence 4, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabria, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 12175890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: human

US-10-850-270-4

Query Match 99.7%; Score 2165; DB 5; Length 427;
Best Local Similarity 99.8%; Pred. No. 3.2e-179;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTETOPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRI 60
Db 27 APTETOPPVNTLSVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRI 86
Qy 61 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
Db 87 EVPLNERICLVGSGQSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 146
Qy 121 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 180
Db 147 LPRGNTSPDNTYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSFQHSVQIMV 206
Qy 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 240
Db 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYVQWENPQNFISRCLFYEVENVN 266
Qy 241 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 300
Db 267 SQTETHNVFVQEAKECNPEFERNVENTSCFMVPGVLPDLTNTVRIRVKTNKLCEYDDKL 326
Qy 301 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 360
Db 327 WSNWSQEMSGKGRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIFPPIDPGKIFK 386
Qy 361 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 401
Db 387 EMFGDQNDTLLHWKKYDIYEKQTKETSDSVLLIENLKASQ 427

RESULT 4

US-10-036-568-4
; Sequence 4, Application US/10036568
; Publication No. US20020090682A1
; GENERAL INFORMATION:


```
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian G.
; TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: Davies cc
; CURRENT APPLICATION NUMBER: US/10/036,568
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US/09/051,843
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4

Query Match      99.2%; Score 2154; DB 4; Length 426;
Best Local Similarity 99.3%; Pred. No. 2.9e-178;
Matches 398; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 60
Db 26 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 85
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 86 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 145
Qy 121 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 146 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 205
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 206 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 265
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
Db 266 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 325
Qy 301 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 360
Db 326 WSNWSQEMTIIVKGRNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 385
Qy 361 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 386 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 426

RESULT 5
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. US20020165135A1
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-036-568-4

Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 124
Qy 121 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 125 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 185 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 244
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
Db 245 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 304
Qy 301 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 360
Db 305 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 364
Qy 361 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 365 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 405
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; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-50

Query Match      86.0%; Score 1869; DB 3; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 124
Qy 121 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 125 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 185 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 244
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
Db 245 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 304
Qy 301 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 360
Db 305 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 364
Qy 361 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 365 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 405

RESULT 6
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heskia Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-753-159-50

Query Match      86.0%; Score 1869; DB 4; Length 405;
Best Local Similarity 85.5%; Pred. No. 1.5e-153;
Matches 343; Conservative 24; Mismatches 34; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 60
Db 5 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASNCSLWYFSHFGDKQDKKIAPETRISI 64
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 65 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 124
Qy 121 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 180
Db 125 LPGNTSPDNTYLYWHSRLEKHOCENIPREGQYFGCSPDLTKVKQSSFEQHSVQIMV 184
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 240
Db 185 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVEVNN 244
Qy 241 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 300
Db 245 SQTETHNVFYVQEAKECENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKL 304
Qy 301 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 360
Db 305 WSNWSQEMSGKGNSTLYITMLLIVPVIVAGAIIVLLYLLKRLKLIIFPPDPGKIFK 364
Qy 361 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 401
Db 365 EMFGDQNDTLHWKKYDIYEKOTKEETDSVVLLENLKKASQ 405
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QY 121 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 180
DB 125 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 184
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 185 KDNARKIRPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 244
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 300
DB 245 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 304
QY 301 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 360
DB 305 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 364
QY 361 EMFGDQNDTLHWKDYIYKQKEETDSVVLJENLKKASQ 401
DB 365 EMFGDQNDTLHWKDYIYKQKEETDSVVLJENLKKASQ 405
RESULT 7
US-10-850-270-10
; Sequence 10, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Fabri, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 121/5890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 664
; TYPE: PRT
; ORGANISM: human
US-10-850-270-10
Query Match 82.2%; Score 1784.5; DB 5; Length 664;
Best Local Similarity 91.7%; Pred. No. 6.5e-146;
Matches 333; Conservative 8; Mismatches 15; Indels 7; Gaps 3;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
DB 45 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 104
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 105 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 164
QY 121 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 180
DB 165 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 224
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 225 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 284
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 300
DB 285 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 344
QY 301 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 354
DB 305 WSNWSQEMSGKKNSTLYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 354

DB 345 WSNWSQEMSGKKNSTGEIE-AIVVPVCLAFLLTLLGLVLCFCKNEDLKKIHWPNVPD 403
QY 355 PGK 357
DB 404 PSK 406
RESULT 8
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36
Query Match 80.6%; Score 1750; DB 3; Length 776;
Best Local Similarity 90.7%; Pred. No. 8e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 14; Gaps 2;
QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 60
DB 232 APTETOPPVTNLVSVENLCTVIWTWNPPEGASNSCLWYFHFHFGDKQDKKIAPETRRSI 291
QY 61 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 120
DB 292 EVPLNERICLVQSGQCSSTNESEKPSILVEKICISPPGDPESAVTELCIWHNLSYMKCSW 351
QY 121 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 180
DB 352 LPRGNTSPDNTYLYYHRSLEKIHOCEINIFREGQVFGCSFDLTWKVDSSFEQHSQIWMV 411
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 240
DB 412 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 471
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 300
DB 472 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDNLTVIRVKTNKLKYEDDKL 531
QY 301 WSNWSQEMSGKKNST--LYITMLLIVPVIVAGAIIVLLLYLKLKIIIFPPIP 353
DB 532 WSNWSQEMSGKKNSTGDKTHTCPCPAPELLGSP-----SVPLFFPKP 576

RESULT 9
US-09-313-942-30
; Sequence 30, Application US/09313942
; Publication No. US2002012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match      80.5%; Score 1749.5; DB 3; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 298
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 478
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 10
US-09-935-868-30
; Sequence 30, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-30

Query Match      80.5%; Score 1749.5; DB 3; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 298
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 478
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 11
US-10-287-035-30
; Sequence 30, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Vancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-30

Query Match      80.5%; Score 1749.5; DB 4; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

Qy 1 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 60
Db 239 APTETQPPVTNLSVSVENLCTVIWTPNPPEGASNCSLWYFSHFQDQKQKIAPETRISI 298
Qy 61 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQVGSQCSTNESEKPSILVEKICISPPGDPESAVTELOCIWHNLSYMKCSW 358
Qy 121 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 180
Db 359 LPRGNTSPDNTYLYWHRSLRLEKIHQENIFREGQYFGCSFDLTWKVDSSFEQHSQVIMV 418
Qy 181 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 240
Db 419 KDNAGKIKPSFNIIVPLTSRVKPDPPHINKLSFHNDDLYVQWENPQNFISRCLFYVEVEVNN 478
Qy 241 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDNTLVIRVKTNKLKYEDDKL 538
Qy 301 WSNWSQEMSIGKRNST-----LYITMLLIIVPVIIVAGAIIVLLLYLKLKLIIFPPIP 353
Db 539 WSNWSQEMSIGKRNSTGDKTHTCCPCPAPELLGGP-----SVFLFPPKP 584

RESULT 12
US-10-282-162-30
; Sequence 30, Application US/10282162
; Publication No. US20030143697A1
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; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: 2003-05-20
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30

Query Match      80.5%; Score 1749.5; DB 4; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 298
QY 61 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 358
QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 359 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLTVQWENPQNFISRCIFYEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLTVQWENPQNFISRCIFYEVEVNN 478
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 538
QY 301 WSNWSQEMSGKGRNST-----LYITMLLIVPVIAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSGKGRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 13
US-11-134-114-30
; Sequence 30, Application US/11/134,114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 2003C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-30

Query Match      80.5%; Score 1749.5; DB 6; Length 784;
Best Local Similarity 90.5%; Pred. No. 8.9e-143;
Matches 323; Conservative 5; Mismatches 14; Indels 15; Gaps 2;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 239 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 298
QY 61 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 120
Db 299 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 358
QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
Db 359 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 418
QY 181 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLTVQWENPQNFISRCIFYEVEVNN 240
Db 419 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLTVQWENPQNFISRCIFYEVEVNN 478
QY 241 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 300
Db 479 SQTETHNVFVQBAKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLKYEDDKL 538
QY 301 WSNWSQEMSGKGRNST-----LYITMLLIVPVIAGAIIVLLLYLRLKLIIPPPIP 353
Db 539 WSNWSQEMSGKGRNSTTGDKTHTCCPAPPELLGGP-----SVFLFPPKP 584

RESULT 14
US-09-825-561A-82
; Sequence 82, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82

Query Match      80.3%; Score 1745; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.6e-143;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 60
Db 6 APTETOPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 65
QY 61 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 120
Db 66 EVPLNERICLVQVSGQCSSTNESEKPSILVEKICISPPGDPESAATVETLQCIWHNLSYMKCSW 125
QY 121 LPCRNTSPDNTNYLYYWHRSLEKIHOCENIFREGQYFGCSFDLTWKVDSSFEQHSQIWMV 180
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Search completed: February 8, 2006, 22:34:53
Job time : 109.728 secs

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Db 126 LFGRTSPDNTYLYYHRSLEKIHQCENIFREGQYFGCSFDLTAKVXDSSFEQHSVQIMV 185
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVVNN 240
Db 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVVNN 245
Qy 241 SOTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 246 SOTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 305
Qy 301 WSNWSQEMSIGKKRNST 317
Db 306 WSNWSQEMSIGKKRNST 322
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RESULT 15
US-10-872-087-82
; Sequence 82, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1
; CURRENT APPLICATION NUMBER: US/10/872,087
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/825,561
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-82
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Query Match 80.3%; Score 1745; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.6e-143;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKODKKIAPETRSI 60
Db 6 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLWYFSHFQDKODKKIAPETRSI 65
Qy 61 EVDPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPPEAVTELCIWHNLSYMKCSW 120
Db 66 EVDPLNERICLVGSCQSTNESEKPSILVEKICISPPGDPPEAVTELCIWHNLSYMKCSW 125
Qy 121 LFGRTSPDNTYLYYHRSLEKIHQCENIFREGQYFGCSFDLTAKVXDSSFEQHSVQIMV 180
Db 126 LFGRTSPDNTYLYYHRSLEKIHQCENIFREGQYFGCSFDLTAKVXDSSFEQHSVQIMV 185
Qy 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVVNN 240
Db 186 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHNDLLVQWENPQNFISRCLFYEVVNN 245
Qy 241 SOTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 300
Db 246 SOTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDTLNTVIRVKTNKLCEYDDKL 305
Qy 301 WSNWSQEMSIGKKRNST 317
Db 306 WSNWSQEMSIGKKRNST 322
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OM protein - protein search, using sw model

Run on: February 8, 2006, 22:29:50 ; Search time 8.74019 Seconds
(without alignments)
602.062 Million cell updates/sec

Title: US-10-036-568A-4_COPY_26_426

Perfect score: 2172

Sequence: 1 APTETQPPVTNLVSVENLCT.....QTKETDSVVLLENLKKASQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2172	100.0	427	US-11-185-230-4	Sequence 4, Appli
2	1679.5	77.3	424	US-11-185-230-6	Sequence 6, Appli
3	296.5	13.7	420	US-11-185-230-5	Sequence 5, Appli
4	294.5	13.6	380	US-10-989-313-4	Sequence 4, Appli
5	294.5	13.6	380	US-11-185-230-2	Sequence 2, Appli
6	293.5	13.5	378	US-11-185-230-2	Sequence 12, Appli
7	287.5	13.2	383	US-10-989-313-2	Sequence 2, Appli
8	230	10.6	313	US-11-193-512-106	Sequence 106, App
9	202	9.3	341	US-10-511-722-21	Sequence 21, Appli
10	202	9.3	357	US-10-511-722-20	Sequence 20, Appli
11	202	9.3	369	US-11-105-268-60	Sequence 60, Appli
12	178.5	8.2	411	US-11-075-351-47	Sequence 47, Appli
13	173	8.0	646	US-10-995-561-695	Sequence 695, App
14	173	8.0	708	US-10-636-320-2	Sequence 2, Appli
15	173	8.0	918	US-10-995-561-696	Sequence 696, App
16	168.5	7.8	329	US-10-995-561-694	Sequence 694, App
17	168	7.7	897	US-11-124-367A-449	Sequence 449, App
18	168	7.7	897	US-11-124-367A-451	Sequence 451, App
19	166	7.6	903	US-11-124-367A-450	Sequence 450, App
20	125	5.8	825	US-10-995-561-679	Sequence 679, App
21	125	5.8	825	US-11-124-367A-469	Sequence 469, App
22	125	5.8	852	US-11-104-923A-5	Sequence 5, Appli
23	113	5.2	631	US-10-813-646-22	Sequence 22, Appli
24	111.5	5.1	979	US-10-636-320-6	Sequence 6, Appli
25	107.5	4.9	360	US-11-084-408-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vitca, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4

Query Match	100.0%	Score 2172;	DB 7;	Length 427;
Best Local Similarity	100.0%	Pred. No. 2.3e-184;		
Matches 401;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	APTETQPPVTNLVSVENLCTVIWTNPPEGASNCSLWYFSHFQDKQDKKIAPETRISI	60	
DB	27	APTETQPPVTNLVSVENLCTVIWTNPPEGASNCSLWYFSHFQDKQDKKIAPETRISI	86	
QY	61	EVPLNERICLVGSGCSTNESEKSIIVKICISPEGPESAVTELQCIWHNLSYMKCSW	120	
DB	87	EVPLNERICLVGSGCSTNESEKSIIVKICISPEGPESAVTELQCIWHNLSYMKCSW	146	
QY	121	LPGRNTSPDTNLTYYHRSLEKIHQCNIFREGYFGCSFDLTVKVDDSSPQHSVQIMV	180	
DB	147	LPGRNTSPDTNLTYYHRSLEKIHQCNIFREGYFGCSFDLTVKVDDSSPQHSVQIMV	206	
QY	181	KDNAGKIPSFNIVPLTSRVKPDPPHINKLSFNHNDLTVQWENPNQFISRCIFYEVVNN	240	
DB	207	KDNAGKIPSFNIVPLTSRVKPDPPHINKLSFNHNDLTVQWENPNQFISRCIFYEVVNN	266	
QY	241	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDLTNTVIRKTNKLCYEDDKL	300	
DB	267	SQTETHNVFYVQEAACENPEFERNVENTSCFMVPGVLPDLTNTVIRKTNKLCYEDDKL	326	

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QY 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 360
Db 327 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 386
QY 361 EMFGDQNDTLHWKKYDIYKQTKETDSVVLLENLKASQ 401
Db 387 EMFGDQNDTLHWKKYDIYKQTKETDSVVLLENLKASQ 427

RESULT 2
US-11-185-230-6
; Sequence 6, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; PRIOR FILING DATE: 2005-07-18
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT 3
; ORGANISM: Mus musculus
; FEATURE:
US-11-185-230-6

Query Match 77.3%; Score 1679.5; DB 7; Length 424;
Best Local Similarity 77.0%; Pred. No. 6.9e-141;
Matches 308; Conservative 40; Mismatches 51; Indels 1; Gaps 1;

QY 1 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRISI 60
Db 25 APTETQPPVNLVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRISKE 84
QY 61 EVPLNERICLVQSCSTNESEKPSILVEKICIPPEGDPESAVTELQCIWHNLSYMKCSW 120
Db 85 ELPLDEKICLVQSCSTNESEKPSILVEKICIPPEGDPESAVTELQCIWHNLSYMKCSW 144
QY 121 LPGRTNSPDNTYLYYWHRSLEKIHQENIFREGQVFGCSFDLTWKVDSFEQHSVQIMV 180
Db 145 LPGRTNSPDNTYLYYWHRSLEKIHQENIFREGQVFGCSFDLTWKVDSFEQHSVQIMV 203
QY 181 KDNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHNDLIVQWENPQNFISRLCFYEVEVNN 240
Db 204 KDNAGKIRPSCKIVSLTSYVVKPDPPHINKLLKNGALLVQWKNPQNFISRLCFYEVEVNN 263
QY 241 SQTETHNVFVVOAKCENPERFERNVTSFCFVPGVLPDNTLVTRVTKNLCYEDDKL 300
Db 264 TQDRHILEVEDKQNSDSRNMGTSCFQLPGLADAVYTRVRVTKNLCYEDDKL 323
QY 301 WSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIDPGKIFK 360
Db 324 WSDWSEASQISGKQNSFTYITMLLITPVFAVAIVILLFYLKRLKIIIFPPIDPGKIFK 383
QY 361 EMFGDQNDTLHWKKYDIYKQTKETDSVVLLENLKAS 400
Db 384 EMFGDQNDTLHWKKYDIYKQTKETDSVVLLENLKAA 423

RESULT 3
US-11-185-230-5
; Sequence 5, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
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; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 420
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-5

Query Match 13.7%; Score 296.5; DB 7; Length 420;
Best Local Similarity 24.8%; Pred. No. 8.5e-19;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 7 PPVTNLSVSVENLCTVIWTWNPPEGASNSCLWYFSGDKQDKKIAPETRISIEVPLN 65
Db 32 PPV-NFTIKVTGLAQVLLQWKNPDQEQRVNLEY-----QVKINAPK-EDDYETRI 82
QY 66 ERICLVQ-----GSQCSTNESEKPSILVEKICIS-----PPEGDPESAVTELQCIWHNL--- 113
Db 83 ESKCVTLHKGFSGASVRTILQNDHSLASSWASAEHLAPGSPGTSIVNLTCITNTTNDN 142
QY 114 -----SY-----MKCSWLPGRNTSPDNTYLYYWHRSLEKIHQENIPRE--GOYFGCSFDL 163
Db 143 YSLRSYQSLHCTWLVDAPEDTQYFLYRYSWTE--ECQEYKDTLGRNIACWPPR 200
QY 164 TKYKDSSEFQHSVQIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFNHNDLIVQWEN 223
Db 201 TPILSKGRDWLSVLVNGSSKHSARPPDQLFALHAIDQINPPLNVAEISGTRLSIQWEK 260
QY 224 PQN-FISRLCFYEVEVNNQSTETHNVFVVOAKCENPERFERNVTSFCFVPGVLPDNTLN 282
Db 261 PVSAPFTIHCDFYEVKIHTRNG-----YLIQEKLMTNAFISIIDLSKY----- 304
QY 283 TVRIRVTKNLCYEDDKLMSNWSQMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLK 342
Db 305 DVQVRAAVSMCKEAG-LMSEWSQPIYVGNDEKHPREWFVIVIMATICIFILILSLICK 363
QY 343 --RLKIIIFPPIDPGKIFKEMFGDQNDTLHWKKYDIYKQTKETDSVVL 392
Db 364 ICHLWIKLFPPIPAKSNIKDLFVTTN-----YEKAGSSETEIEVI 404

RESULT 4
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 380
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Qy 129 DTNTYLYYHRSLEKIHQC-ENIFREGQYFGCSFDLTVKVDSSPEQHSVQIMVKDNAGKI 181
Db 166 DTNTNLFYFYEGDHALQCVDYIKADGQNIKGRFPYLEASD--YKDFYICVNGSSSENKPI 223

Qy 188 KPSFNIVPLTSRVKPPDPHPHIKNLSFHDN---DLVYQWENPQNFI-SRCLFYEVEVNNST 243
Db 224 RSYFTFQIQNIYKPLPP--VYLFTTRSSCEIKLWISIPLGPIPARCFDYEIREDDT 281

Qy 244 ETHNVFYVQAKCENPEFERNVENTS---CFMVPGVLPTDLNTVIRVKTNKLCEYDDKL 300
Db 282 T-----LVATVATENETYLKTTNETRQLCFV-----RSKNVIYC-SDDGI 321

Qy 301 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIAGAIIVLLLYLKLKLIIRPPI 355
Db 322 WSEWSDKQCEWGBDLSKTLRLFWLPF-----GFILILVIFVTGL---LRLKPNTYP 370

Qy 356 GKIPKEMFGD 365
Db 371 -KMIPEFFCD 379

RESULT 6
US/11/185
; Sequence 12, Application US/111185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 378
; TYPE: PRT 3
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is
US/11/185,230-12

Query Match 13.5%; Score 293.5; DB 7; Length 378;
Best Local Similarity 27.5%; Pred. No. 1.4e-18;
Matches 94; Conservative 55; Mismatches 130; Indels 63; Gaps 18

Qy 26 WNPPEGAS--SNCSLWYFSHFQDKDKKIAPETRRI-----EVLNERICLVQGS 74
Db 53 WQPLSLDHPKCEVY-----ELKYRNISETWKTIIITKNLHYKDGFDLNLKGIKAIHT 107

Qy 75 ----QCSTNESEKPSILVEKC--ISPPGDEBSATELQCIWHNLSYMKCSWLPGRNTSP 128
Db 108 LLPQC-TNGSEVQSSWAETTYWIS-POGIPETKYQDMDCVYINNYQLLCSWKPGIGVLL 165

Qy 129 DTNTYLYYHRSLEKIHQC-ENIFREGQYFGCSFDLTVKVDSSPEQHSVQIMVKDNAGKI 187
Db 166 DTNTNLFYFYEGDHALQCVDYIKADGQNIKGRFPYLEASD--YKDFYICVNGSSSENKPI 223

Qy 188 KPSFNIVPLTSRVKPPDPHPHIKNLSFHDN---DLVYQWENPQNFI-SRCLFYEVEVNNST 243
Db 224 RSYFTFQIQNIYKPLPP--VYLFTTRSSCEIKLWISIPLGPIPARCFDYEIREDDT 281

Qy 244 ETHNVFYVQAKCENPEFERNVENTS---CFMVPGVLPTDLNTVIRVKTNKLCEYDDKL 300
Db 282 T-----LVATVATENETYLKTTNETRQLCFV-----RSKNVIYC-SDDGI 321

Qy 301 WSNWSQEM-----SIGKRNSTLYIT--MLLIVPVIAGAI 335
Db 322 WSEWSDKQCEWGBDLSKTLRLFWLPFGFILILVIFVTGLL 363

```

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RESULT 7
US-10-989-313-2
; Sequence 2, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lora
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; APPLICANT: Wills-Karp, Marsha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: Cytokine Receptor Chain
; FILE REFERENCE: GI 5268A
; CURRENT APPLICATION NUMBER: US/10/989,313
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/868,123
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-989-313-2

Query Match      13.2%; Score 287.5; DB 6; Length 383;
Best Local Similarity 25.6%; Pred. No. 4.7e-18;
Matches 89; Conservative 54; Mismatches 156; Indels 49; Gaps 14;

QY 26 WNP-----EGASSNCSLWYFHFSGDKQDKKIAPETRRSIEVPLNE-----RICLQVGSQ 75
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 47 WKPVPVLEKPKGCTLELYELKYRNVDSDSWKTIITRNLYYKDGFDLNGIGKIRTHLSEH 106
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 76 CSTNESEKPSILIVEKICIS--PPEGDPESAVTELOCIWHNLSYMKCSMLPGRNTSPDNTNYTL 134
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 107 C-TNGSEVQSPWIEASGYISDEGSLETQIQDKCIYNNQWLYVCSWKPKGTIVYSDNTNYTM 165
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 135 YYWHRSLKTHQCENTIFR-EGQVFGCSFDLTQVKDSSFEQHSQVIMVKDNAGKIKPSFNI 193
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 166 FFWYEGDLHALQADYLOHDEKVGCK--LSNLDSSDYKDFFCVNGSKLEPIRSYTV 223
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 194 VPITSRVKPDPPIHKNLSFND-DLYVQWENPQNF1-SRCLFYEVENNSQTETHNVFYV 251
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 224 FQLQNIWKPLPPEFLHISVENSIDIRMKWSTPGPIPPRCYTYEIVIREDDISWESATDK 283
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 252 QEAKCENPEPERNVNTSCFMVPGVLPDTLNTVIRVKTNKLCEYEDDKLWSNQEMS-- 309
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 284 NDKLKR--RANESEDLCPFV-----RCKVNIYC-ADGGIMSEWSBECEWE 326
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 310 --IGKRNSTLYITMLLIIVPVIAGATIVLLYLKRLKIIPPIPPDP 355
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 327 GYTGPDSK-----IIFIVPVCLFFILLLLCL-----IVEKEBEP 363
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 8
US-11-193-512-106
; Sequence 106, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akibiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, Nobuo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-Aug-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-869-9741
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-11-193-512-106
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Query Match      10.6%; Score 230; DB 7; Length 313;
Best Local Similarity 24.8%; Pred. No. 4.4e-13;
Matches 82; Conservative 51; Mismatches 145; Indels 52; Gaps 14;

QY 7 PPVTNLSVSVENLCTVIWTNW-PGASNSCSLWYFHFSGDKQDKKIAPETRRSIEVPLN 65
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 12 PPV-NFTIKVTGLAQVLLQWKNPDQQRNVNLEY-----QVKINAPK-EDDYETRIT 62
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 66 ERICLV-----GSQCSTNESEKPSILIVEKICIS-----PPEGDPESAVTELOCIWHNL--- 113
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 63 ESKCVTILHKGFSAVVRTILQNDHSLASSWASAEHLHAPPGSPGVNLTCTTNTEDN 122
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 114 -----SY-----MKCSWLPGRNTSPDNTNYLYWHRSLKTHQCENTIFR--GOYFGCSFDL 163
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 123 YSLRSYQVSLHCTWLVGDAPEDTQYFLYRYGSWTE--ECQEYSKDTLGRNIACWFR 180
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 164 TRVKDSSFQHSYQVIMVKDNAGKIKPSFNIPLVTSRVKPDPPHKNLSFNDLQVQWEN 223
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 181 TPILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNLTAEIETRLSIQWEK 240
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 224 PQN-FISRCLFYEVENNSQTETHNVFYVQEAKECENPEPERNVNTSCFMVPGVLPDTLN 282
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 241 PVSAPFIHCFDYEYKIHNRNG-----YIQIEKLMTNAFIISIIDLISKY----- 284
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 283 TVRIRVKTNKLCEYEDDKLWSNQEMSIGK 312
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 285 DVQVRAAVSMCKEAG-LMSEWSQPIYVGK 313
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

```
RESULT 9
US-10-511-722-21
; Sequence 21, Application US/10511722
```


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